

Sequence Alignment

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 9, 2005, 23:46:53 ; Search time 40 Seconds
(without alignments)
921.276 Million cell updates/sec

Title: US-10-056-405-2
Perfect score: 383
Sequence: 1 MVYNFKVKKCAPNGKVTLY.....ADVERTPRQDTIDQASVDPE 383

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : PIR_79:*\n1: p1r1:*\n2: p1r2:*\n3: p1r3:*\n4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	5.2	364	2 A34867	arrestin - fruit f
2	17	4.4	363	2 A55081	arrestin 1 - blueb
3	16	4.2	381	2 B56607	arrestin homolog -
4	12	3.1	407	2 A56607	arrestin homolog -
5	11	2.9	401	2 A34856	49K photoreceptor
6	11	2.9	401	2 S11566	arrestin homolog -
7	11	2.9	401	2 B55081	arrestin 2 - blueb
8	11	2.9	405	2 S68254	arrestin isoform 2
9	11	2.9	407	2 S68253	arrestin isoform 1
10	11	2.9	409	2 S18984	arrestin - human (
11	11	2.9	410	2 A59279	beta-arrestin 2 -
12	11	2.9	415	2 S68255	arrestin isoform 1
13	11	2.9	420	2 A47140	arrestin arr3L - b
14	9	2.3	387	2 I55423	arrestin-C - human
15	9	2.3	388	2 S38943	arrestin - human
16	9	2.3	1773	2 T05128	hypothetical prote
17	8	2.1	403	2 J80066	S-antigen - mouse
18	8	2.1	403	2 S03960	S-antigen - rat
19	8	2.1	404	2 A28404	S-antigen - bovine
20	8	2.1	405	2 A30357	retinal S-antigen
21	8	2.1	412	2 F87709	DNA/pantothenate m
22	8	2.1	418	2 B46682	beta-arrestin 1, s
23	8	2.1	418	2 A34851	beta-arrestin, bra
24	8	2.1	418	2 B43404	beta-arrestin1 - r
25	8	2.1	448	2 D71852	probable signal re
26	8	2.1	448	2 H64663	signal recognition
27	7	1.8	53	2 AF2764	nitrogen fixation
28	7	1.8	57	2 P70202	protein-tyrosine k
29	7	1.8	83	1 MSWLHS	E5 protein - human

30	7	1.8	92	2 B82603	hypothetical prote
31	7	1.8	111	2 S10222	hypothetical prote
32	7	1.8	139	2 E97426	flagellar basal-bo
33	7	1.8	139	2 AE2644	flagellar basal-bo
34	7	1.8	142	2 F81048	conserved hypothet
35	7	1.8	145	2 C64447	hypothetical prote
36	7	1.8	149	2 A87346	hypothetical prote
37	7	1.8	151	2 A83639	osmotically induci
38	7	1.8	155	2 C81827	hypothetical prote
39	7	1.8	161	2 A27873	allophycocyanin a1
40	7	1.8	166	2 A95969	hypothetical prote
41	7	1.8	174	2 S39877	caro protein - Myx
42	7	1.8	216	2 A61259	glycoprotein S - p
43	7	1.8	217	2 B64080	hypothetical prote
44	7	1.8	231	2 S73469	probable lipoprote
45	7	1.8	231	2 A82084	MTR/SAH nucleosida

ALIGNMENTS

RESULT 1

A34867
arrestin - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 09-Jul-2004
C:Accession: A34867; A34868
R:Smith, D.P.; Shieh, B.H.; Zuker, C.S.
Proc. Natl. Acad. Sci. U.S.A. 87, 1003-1007, 1990
A:Title: Isolation and structure of an arrestin gene from Drosophila.
A:Reference number: A34867; MUID:90138925; PMID:1689056
A:Accession: A34867
A:Status: preliminary
A:Molecule type: DNA
A:Molecule type: DNA
A:Residues: 1-364 <SMI>
A:Cross-references: UNIPROT:P15372; GB:M30177
R:Hyde, D.R.; Mecklenburg, K.L.; Pollock, J.A.; Vahetelc, T.S.; Benzer, S.
Proc. Natl. Acad. Sci. U.S.A. 87, 1008-1012, 1990
A:Title: Twenty Drosophila visual system cDNA clones: one is a homolog of human arrestin
A:Reference number: A34868; MUID:90138926; PMID:2105491
A:Accession: A34868
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-364 <HYD>
A:Cross-references: GB:M30140; NID:g156961; PIDN:AAA28380.1; PID:g156962
C:Genetics:
A:Gene: FlyBase:Arr1
A:Cross-references: FlyBase:FBgn0000120
A:Introns: 36/3; 306/3; 349/3
C:Superfamily: arrestin

Query Match 5.2%; Score 20; DB 2; Length 364;
Best Local Similarity 100.0%; Pred. No. 3e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 228 VKKIKAMVQGVDPVLFQNG 247
Db 227 VKKIKAMVQGVDPVLFQNG 246

RESULT 2
A55081
arrestin 1 - bluebottle fly (Calliphora vicina)
C:Species: Calliphora vicina
C>Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C:Accession: A55081; S44291
R:Planger, A.; Malicki, D.; Whitney, M.; Paulsen, R.
J. Biol. Chem. 269, 26969-26975, 1994
A:Title: Mechanism of arrestin 2 function in rhabdomic photoreceptors.
A:Reference number: A55081; MUID:95014564; PMID:7929436
A:Accession: A55081
A:Status: preliminary
A:Molecule type: mRNA

This Page Blank (uspto)

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 9, 2005, 23:46:53 ; Search time 40 Seconds
(without alignments)
921.276 Million cell updates/sec

Title: US-10-056-405-2
Perfect score: 383
Sequence: 1 MVMNFKVFKKCAPNGKVTLY.....ADVETFRQDTIDQASVDFE 383

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	5.2	364	2 A34867	arrestin - fruit f
2	17	4.4	363	2 A55081	arrestin 1 - blueb
3	16	4.2	381	2 B56607	arrestin homolog -
4	12	3.1	407	2 A56607	arrestin homolog -
5	11	2.9	401	2 A34856	49K photoreceptor
6	11	2.9	401	2 S11566	arrestin homolog -
7	11	2.9	401	2 B55081	arrestin 2 - blueb
8	11	2.9	405	2 S68254	arrestin isoform 2
9	11	2.9	407	2 S68253	arrestin isoform 1
10	11	2.9	409	2 S18984	arrestin - human (
11	11	2.9	410	2 A59279	beta-arrestin 2 -
12	11	2.9	415	2 S68255	arrestin isoform 1
13	11	2.9	420	2 A47140	arrestin arr3l - b
14	9	2.3	387	2 I55423	arrestin-C - human
15	9	2.3	388	2 S38943	arrestin - human
16	9	2.3	1773	2 T05128	hypothetical prote
17	8	2.1	403	2 JS0066	S-antigen - mouse
18	8	2.1	403	2 S03960	S-antigen - rat
19	8	2.1	404	2 A28404	S-antigen - bovine
20	8	2.1	405	2 A30357	retinal S-antigen
21	8	2.1	412	2 F87709	DNA/pantothenate m
22	8	2.1	418	2 B46682	beta-arrestin 1, s
23	8	2.1	418	2 A34851	beta-arrestin, bra
24	8	2.1	418	2 B43404	beta-arrestin1 - r
25	8	2.1	448	2 D71852	probable signal re
26	8	2.1	448	2 H64663	signal recognition
27	7	1.8	53	2 AF2764	nitrogen fixation
28	7	1.8	57	2 PT0202	protein-tyrosine k
29	7	1.8	83	1 W5WLHS	E5 protein - human

30	7	1.8	92	2 B82603	hypothetical prote
31	7	1.8	111	2 S10222	hypothetical prote
32	7	1.8	139	2 E97426	flagellar basal-bo
33	7	1.8	139	2 AE2644	flagellar basal-bo
34	7	1.8	142	2 F81048	conserved hypochet
35	7	1.8	145	2 C64447	hypothetical prote
36	7	1.8	149	2 A87346	hypothetical prote
37	7	1.8	151	2 A83639	osmotically induc
38	7	1.8	155	2 C81827	hypothetical prote
39	7	1.8	161	2 A27873	allophycocyanin al
40	7	1.8	166	2 A95969	hypothetical prote
41	7	1.8	174	2 S39877	carq protein - Myx
42	7	1.8	216	2 A61259	glycoprotein S - p
43	7	1.8	217	2 B64080	hypothetical prote
44	7	1.8	231	2 S73469	probable lipoprote
45	7	1.8	231	2 A82084	MTA/SAH nucleosida

ALIGNMENTS

RESULT 1
A34867
arrestin - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 09-Jul-2004
C:Accession: A34867; A34868
R:Smith, D.P.; Shieh, B.H.; Zuker, C.S.
Proc. Natl. Acad. Sci. U.S.A. 87, 1003-1007, 1990
A:Title: Isolation and structure of an arrestin gene from Drosophila.
A:Reference number: A34867; MUID:90138925; PMID:1689056
A:Accession: A34867
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-364 <SMI>
A:Cross-references: UNIPROT:P15372; GB:M30177
R:Hyde, D.R.; Mecklenburg, K.L.; Pollock, J.A.; Vihetic, T.S.; Benzer, S.
Proc. Natl. Acad. Sci. U.S.A. 87, 1008-1012, 1990
A:Title: Twenty Drosophila visual system cDNA clones: one is a homolog of human arrestin
A:Reference number: A34868; MUID:90138926; PMID:2105491
A:Accession: A34868
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-364 <HYD>
A:Cross-references: GB:M30140; NID:g156961; PIDN:AAA28380.1; PID:g156962
C:Genetics:
A:Gene: FlyBase:Arr1
A:Cross-references: FlyBase:FBgn0000120
A:Introns: 36/3; 306/3; 349/3
C:Superfamily: arrestin

Query Match 5.2%; Score 20; DB 2; Length 364;
Best Local Similarity 100.0%; Pred. No. 3e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 228 VKKIKAMVQGGVDVLFONG 247
Db 227 VKKIKAMVQGGVDVLFONG 246

RESULT 2
A55081
arrestin 1 - bluebottle fly (Calliphora vicina)
C:Species: Calliphora vicina
C:Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C:Accession: A55081; S44291
R:Plangger, A.; Malicki, D.; Whitney, M.; Paulsen, R.
J. Biol. Chem. 269, 26969-26975, 1994
A:Title: Mechanism of arrestin 2 function in rhabdomic photoreceptors.
A:Reference number: A55081; MUID:95014564; PMID:7929436
A:Accession: A55081
A:Status: preliminary
A:Molecule type: mRNA

A;Residues: 1-363 <PLA>
A;Cross-references: UNIPROT:P51486; GB:X79072; NID:G483527; PIDN:CAA55672.1; PID:G483528
A;Note: the source is designated as Calliphora erythrocephala
C;Superfamily: arrestin

Query Match

Best Local Similarity 4.4%; Score 17; DB 2; Length 363;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 322 SYAVKVKFLGALGSEL 338
Db 321 SYAVKVKFLGALGSEL 337
|||||

RESULT 3

B56607
arrestin homolog - tobacco budworm
C;Species: Heliothis virescens (tobacco budworm)
C;Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 09-Jul-2004
R;Ramling, K.; Freitag, J.; Krieger, J.; Breer, H.
A;Title: Arrestin-subtypes in insect antennae.
A;Accession: B56607
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: mRNA
A;Residues: 1-381 <RAM>
A;Cross-references: UNIPROT:P55274
A;Experimental source: antennae
A;Note: sequence extracted from NCBI backbone (NCBIF:127926)
C;Superfamily: arrestin

Query Match

Best Local Similarity 4.2%; Score 16; DB 2; Length 381;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYYNFKVFKKCAPNGK 16
Db 1 MYYNFKVFKKCAPNGK 16
|||||

RESULT 4

A56607
arrestin homolog - migratory locust
C;Species: Locusta migratoria (migratory locust)
C;Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 09-Jul-2004
R;Ramling, K.; Freitag, J.; Krieger, J.; Breer, H.
A;Title: Arrestin-subtypes in insect antennae.
A;Reference number: A56607; MUID:93199955; PMID:8452755
A;Contents: antennae
A;Accession: A56607
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-407 <RAM>
A;Cross-references: UNIPROT:P32122; GB:S57174; NID:G298755; PIDN:AA825860.1; PID:G298756
C;Superfamily: arrestin

Query Match

Best Local Similarity 3.1%; Score 12; DB 2; Length 407;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 RYGREDEVMGL 73
Db 69 RYGREDEVMGL 80
|||||

RESULT 5

A34856
49K photoreceptor protein - fruit fly (Drosophila melanogaster)

C;Species: Drosophila melanogaster
C;Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 09-Jul-2004
C;Accession: A34856
R;Yamada, T.; Takeuchi, Y.; Komori, N.; Kobayashi, H.; Sakai, Y.; Hotta, Y.; Matsunot
Science 248, 483-485, 1990
A;Title: A 49-kilodalton phosphoprotein in the Drosophila photoreceptor is an arresti
A;Reference number: A34856; MUID:90232360; PMID:2158671
A;Accession: A34856
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-401 <YAM>
A;Cross-references: UNIPROT:P19107; GB:M32141; NID:G158157; PIDN:AAA28833.1; PID:G1581
C;Genetics:
A;Gene: FlyBase:Arr2
A;Cross-references: FlyBase:FBgn0000121
C;Superfamily: arrestin

Query Match

Best Local Similarity 2.9%; Score 11; DB 2; Length 401;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 RYGREDEVMG 72
Db 61 RYGREDEVMG 71
|||||

RESULT 6

S11566
arrestin homolog - fruit fly (Drosophila miranda)
C;Species: Drosophila miranda
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
R;Krisnan, R.; Ganguly, R.
Nucleic Acids Res. 18, 5894, 1990
A;Title: Nucleotide sequence of the arrestin-like 49 Kd protein gene of Drosophila miran
A;Reference number: S11566; MUID:91016944; PMID:2216789
A;Accession: S11566
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-401 <KRI>
A;Cross-references: UNIPROT:P19108; EMBL:X54084; NID:G7612; PIDN:CAA38019.1; PID:G295739
C;Genetics:
A;Gene: FlyBase:Dmir/Arr2
A;Cross-references: FlyBase:FBgn0012552
C;Intons: 286/1; 351/1
C;Superfamily: arrestin

Query Match

Best Local Similarity 2.9%; Score 11; DB 2; Length 401;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 RYGREDEVMG 72
Db 61 RYGREDEVMG 71
|||||

RESULT 7

B55081
arrestin 2 - bluebottle fly (Calliphora vicina)
C;Species: Calliphora vicina
C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
R;Plangger, A.; Malicki, D.; Whitney, M.; Paulsen, R.
J. Biol. Chem. 269, 26969-26975, 1994
A;Title: Mechanism of arrestin 2 function in rhabdomeric photoreceptors.
A;Reference number: A55081; MUID:95014564; PMID:7929436
A;Accession: B55081
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-401 <PLA>
A;Cross-references: UNIPROT:P51487; EMBL:X79073; NID:G483583; PIDN:CAA55673.1; PID:G48358
A;Note: the source is designated as Calliphora erythrocephala
C;Superfamily: arrestin

Query Match 2.9%; Score 11; DB 2; Length 401;
Best Local Similarity 100.0%; Pred. No. 0.0068;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 62 RYGREDEVMG 72
|||||
Db 61 RYGREDEVMG 71

RESULT 8
868254
arrestin isoform 2S, erythrocyte - rainbow trout
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S68254
R;Jahn, R.; Borgee, F.; Lindenthal, S.; Straub, A.; Motaïs, R.; Fievet, B.
Biochem. J. 316, 497-506, 1996
A;Title: Trout red blood cell arrestin (TRCarr), a novel member of the arrestin family:
A;Reference number: S68253; MUID:96257743; PMID:8687393
A;Accession: S68254
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-405 <JAH>
A;Cross-references: UNIPROT:P51467; GB:U48410
C;Superfamily: arrestin

Query Match 2.9%; Score 11; DB 2; Length 405;
Best Local Similarity 100.0%; Pred. No. 0.0068;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 341 ELPFVLMHPKP 351
|||||
Db 339 ELPFVLMHPKP 349

RESULT 9
S68253
arrestin isoform 1S, erythrocyte - rainbow trout
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S68253
R;Jahn, R.; Borgee, F.; Lindenthal, S.; Straub, A.; Motaïs, R.; Fievet, B.
Biochem. J. 316, 497-506, 1996
A;Title: Trout red blood cell arrestin (TRCarr), a novel member of the arrestin family:
A;Reference number: S68253; MUID:96257743; PMID:8687393
A;Accession: S68253
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-407 <JAH>
A;Cross-references: UNIPROT:P51466; GB:U48410; NID:G1215723; PIDN:ABA16954.1; PID:G12157
C;Superfamily: arrestin

Query Match 2.9%; Score 11; DB 2; Length 407;
Best Local Similarity 100.0%; Pred. No. 0.0068;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 341 ELPFVLMHPKP 351
|||||
Db 339 ELPFVLMHPKP 349

RESULT 10
S18984
arrestin - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S18984
R;Rapoport, B.
submitted to the EMBL Data Library, November 1991
A;Description: Isolation of a novel cDNA belonging to the arrestin family from human thymocytes
A;Reference number: S18984
A;Accession: S18984

A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-409 <RAP>
A;Cross-references: UNIPROT:P32121; EMBL:Z11501; NID:G28850; PIDN:CAA77577.1; PID:G28851
C;Superfamily: arrestin

Query Match 2.9%; Score 11; DB 2; Length 409;
Best Local Similarity 100.0%; Pred. No. 0.0068;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 341 ELPFVLMHPKP 351
|||||
Db 339 ELPFVLMHPKP 349

RESULT 11
A59279
beta-arrestin 2 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C;Accession: A59279; A43404; I70112
R;Altamadal, H.; Arriza, J.L.; Aoki, C.; Dawson, T.M.; Codina, J.; Kwatra, M.M.; Snyder
submitted to GenBank, August 1995
A;Reference number: A59279
A;Accession: A59279
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-410 <ATT>
A;Cross-references: UNIPROT:P29067; GB:M91590; NID:G949986; PIDN:AAA74460.1; PID:G203104
A;Experimental source: strain Sprague-Dawley; stage adult; tissue type brain; tissue lib
R;Altamadal, H.; Arriza, J.L.; Aoki, C.; Dawson, T.M.; Codina, J.; Kwatra, M.M.; Snyder
J. Biol. Chem. 267, 17882-17890, 1992
A;Title: Beta-arrestin2, a novel member of the arrestin/beta-arrestin gene family.
A;Reference number: A43404; MUID:92388146; PMID:1517224
A;Accession: A43404
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-320, 'A', 322-325, 'A', 327-330, 'A', 332-410 <AT2>
A;Cross-references: GB:M91590; NID:G949986
A;Note: sequence extracted from NCBI backbone (NCBIP:112790)
A;Note: the sequence is revised in GenBank entry RATBARRES2, release 113.0
R;Craft, C.M.; Whitmore, D.H.; Wiechmann, A.F.
J. Biol. Chem. 269, 4613-4619, 1994
A;Title: Cone arrestin identified by targeting expression of a functional family.
A;Reference number: I55423; MUID:94140898; PMID:8308033
A;Accession: I70112
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 295-410 <CRA>
A;Cross-references: EMBL:U03627; NID:G458202; PIDN:AAA17551.1; PID:G458203
C;Superfamily: arrestin

Query Match 2.9%; Score 11; DB 2; Length 410;
Best Local Similarity 100.0%; Pred. No. 0.0068;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 341 ELPFVLMHPKP 351
|||||
Db 340 ELPFVLMHPKP 350

RESULT 12
S68255
arrestin isoform 1L, erythrocyte - rainbow trout
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S68255
R;Jahn, R.; Borgee, F.; Lindenthal, S.; Straub, A.; Motaïs, R.; Fievet, B.
Biochem. J. 316, 497-506, 1996
A;Title: Trout red blood cell arrestin (TRCarr), a novel member of the arrestin family:
A;Reference number: S68253; MUID:96257743; PMID:8687393
A;Accession: S68255
A;Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA
A:Residues: 1-415 <UAH>
A:Cross-references: UNIPROT:P51468; GB:U48410
C:Superfamily: arrestin

Query Match

Best Local Similarity 2.9%; Score 11; DB 2; Length 415;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 341 ELPFVLMHPKP 351
DB 347 ELPFVLMHPKP 357

RESULT 13

A47140

arrestin arr3L - bovine
N:Contains: arrestin arr3S
C:Species: Bos primigenius taurus (cattle)
C>Date: 16-Feb-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
R:Stearns-Marr, R.; Gurevich, V.V.; Goldsmith, P.; Bodine, R.C.; Sanders, C.; Donoso, L.A.
J. Biol. Chem. 268, 15640-15648, 1993
A:Title: Polypeptide variants of beta-arrestin and arrestin3.
A:Reference number: A47140; MUID:93340166; PMID:8340388
A:Accession: A47140
A:Molecule type: mRNA
A:Residues: 1-420 <STE>
A:Cross-references: UNIPROT:P32120; GB:L14641
A:Experimental source: brain
A>Note: sequence extracted from NCBI backbone (NCBIN:136006, NCBI:P136007)
A:Accession: B47140
A:Molecule type: mRNA
A:Residues: 1-362,374-420 <ST2>
C:Comment: This protein plays a role in the regulation of G-protein-coupled receptors.
F:1-362,374-420/Product: arrestin arr3L #status predicted <MAT>
F:1-362,374-420/Product: arrestin arr3S #status predicted <MA2>

Query Match

Best Local Similarity 2.9%; Score 11; DB 2; Length 420;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 341 ELPFVLMHPKP 351
DB 339 ELPFVLMHPKP 349

RESULT 14

I55423

arrestin-C - human
C:Species: Homo sapiens (man)
C>Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 13-Sep-1998
R:Craft, C.M.; Whitmore, D.H.; Wiechmann, A.F.
J. Biol. Chem. 269, 4613-4619, 1994
A:Title: Cone arrestin identified by targeting expression of a functional family.
A:Reference number: I55423; MUID:94140898; PMID:8308033
A:Accession: I55423
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-387 <RES>
A:Cross-references: EMBL:U03626; NID:9458200; PID:9458201
C:Superfamily: arrestin

Query Match

Best Local Similarity 2.3%; Score 9; DB 2; Length 387;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 GKRDVVDHV 30
DB 19 GKRDVVDHV 27

RESULT 15

S38943

arrestin - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004
R:Murakami, A.; Yajima, T.; Sakuma, H.; McLaren, M.J.; Inana, G.
FEBS Lett. 334, 203-209, 1993
A:Title: X-arrestin: a new retinal arrestin mapping to the X chromosome.
A:Reference number: S38943; MUID:94039835; PMID:8224247
A:Accession: S38943
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-388 <MUR>
A:Cross-references: UNIPROT:P36575; GB:S66793; NID:9439830; PIDN:AA828824.1; PID:9439831
C:Superfamily: arrestin

Query Match

Best Local Similarity 2.3%; Score 9; DB 2; Length 388;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 GKRDVVDHV 30
DB 19 GKRDVVDHV 27

Search completed: February 10, 2005, 00:02:18
Job time : 42 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 9, 2005, 23:39:27 ; Search time 41 Seconds
(without alignments)
898.805 Million cell updates/sec

Title: US-10-056-405-2
Perfect score: 1973
Sequence: 1 MVYNFKVFKKCAPNGKVTLY.....ADVETFRQDTIDQASVDFE 383

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1499	76.0	381	2 B56607	arrestin homolog -
2	1384	70.1	364	2 A34867	arrestin - fruit f
3	1335	67.7	363	2 A55081	arrestin 1 - blueb
4	993.5	50.4	407	2 A56607	arrestin homolog -
5	977.5	49.5	401	2 S11566	arrestin homolog -
6	975.5	49.4	401	2 A34856	49K photoreceptor
7	942.5	47.8	401	2 B55081	arrestin 2 - blueb
8	903.5	45.8	418	2 A34851	beta-arrestin, bra
9	903.5	45.8	418	2 B43404	beta-arrestin 1, s
10	891.5	45.2	418	2 B46682	beta-arrestin 1, s
11	887	45.0	420	2 A47140	arrestin ar3L - b
12	882	44.7	409	2 S18984	arrestin - human (
13	871	44.1	407	2 S68253	arrestin isoform 1
14	869.5	44.1	410	2 A59279	beta-arrestin 2 -
15	865	43.8	454	2 T34297	hypothetical prote
16	863	43.7	415	2 S68255	arrestin isoform 1
17	861	43.6	405	2 S68254	arrestin isoform 2
18	810	41.1	387	2 I51404	cone arrestin - Af
19	785.5	39.8	389	2 S68175	cone arrestin - hu
20	784.5	39.8	389	2 S68172	cone arrestin - no
21	783.5	39.7	403	2 JS0066	S-antigen - mouse
22	780.5	39.6	388	2 S38943	arrestin - human
23	775.5	39.3	403	2 S03960	S-antigen - rat
24	768.5	39.0	404	2 A28404	S-antigen - bovine
25	761	38.6	405	2 A30357	retinal S-antigen
26	731.5	37.1	396	2 S68173	rod arrestin - nor
27	731	37.1	387	2 I55423	arrestin-C - human
28	729.5	37.0	396	2 S68174	rod arrestin - bul
29	134	6.8	92	2 I70113	C-arrestin - rat (

30	129	6.5	378	2 T28112	hypothetical prote
31	118.5	6.0	427	2 T23954	hypothetical prote
32	111.5	5.7	364	2 T26507	hypothetical prote
33	111.5	5.7	471	2 T15155	hypothetical prote
34	111.5	5.7	2413	2 S34670	splicing factor PR
35	110.5	5.6	344	2 T33421	hypothetical prote
36	110	5.6	456	2 T29948	hypothetical prote
37	107.5	5.4	312	2 T20949	hypothetical prote
38	107.5	5.4	460	2 T23955	hypothetical prote
39	106.5	5.4	460	2 T33420	hypothetical prote
40	106	5.4	347	2 S31144	myk1 protein - Myco
41	104	5.3	338	2 F87145	ABC transporter AT
42	102.5	5.2	464	2 T16826	hypothetical prote
43	101.5	5.1	1804	2 T34518	nestin - golden ha
44	100	5.1	359	2 B70534	probable ribonucle
45	99.5	5.0	600	2 S65788	Ku antigen 70K cha

ALIGNMENTS

RESULT 1
B56607
arrestin homolog - tobacco budworm
C:Species: Heliothis virescens (tobacco budworm)
C:Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #ext_change 09-Jul-2004
C:Accession: B56607
R:Raming, K.; Freitag, J.; Krieger, J.; Breer, H.
Cell. Signal. 5, 69-80, 1993
A:Title: Arrestin-subtypes in insect antennae.
A:Reference number: A56607; MUID:93199955; PMID:8452755
A:Accession: B56607
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-381 <RAM>
A:Cross-references: UNIPROT:P55274
A:Experimental source: antennae
A>Note: sequence extracted from NCBI backbone (NCBIP:127926)
C:Superfamily: arrestin

Query Match	76.0%; Score 1499; DB 2; Length 381;
Best Local Similarity	72.7%; Pred. No. 7.7e-112;
Matches 277; Conservative 51; Mismatches 51; Indels 2; Gaps 2;	
QY	1 MVYNFKVFKKCAPNGKVTLYMGKRDVHVSQVEPIDGIYVLDEYIRDNKRVFGQIVCS 60
DB	1 MVYNFKVFKKCAPNGKITLYMAKRDFVDHISTVEPIDGVLLDEEYVR-GRKVFQMVCT 59
QY	61 FRYGREDEVMGLNFQKEICLASEQIYPRPEKSKDEQTKQERLLKLGSAIPTFNIS 120
DB	60 FRYGREDEVMGLNFYKEHFLASEQIYPRPEKRNYSRQERLIKLGGAIPRLTVP 119
QY	121 PNAPSVTLQGGEDDNGDPCGVSYVYKIFAGESETDTRHRSSTVTLGIRKIQAFTKQGQ 180
DB	120 PGAPGSYTLQPLEDDGEBRCGVQYVYKIFVGDSEIDRSRSTVALGIRVQYAPAKGPR 179
QY	181 QPCTLVKDFMLSPGELELVTLDKQLYLHGERIGVNICIRNNSMKVKKIKAMVQGVND 240
DB	180 QPCTVVRKDFVLSPGQLEHETLTDKQLYHGETVAVNMVCVRNHSNKVKKIKACIQGVND 239
QY	241 VVLFQNGSVYRNTVASLSTSEGCPIQPGSSLQKVMYLTPLSSNKQRGIALDGOIKRQDQ 300
DB	240 VVLFQNGSVYRNTVASLSTSEGCPIQPGSSLQKVLHPTLAHNRDKRGIALDGOIKRSDT 299
QY	301 CLASTTLAQPDRDAFAGVISYAVKVKLFLGALGSELGSAELPVLMMHPRGTAKAVIHA 360
DB	300 TLAFTTLTLLDDPDQDAFAGVSVYSYSAKVLYLGAISGELVAELPFLMMHPRGK-RVKMIIHA 358
QY	361 DSQADVETFRQDTIDQASVD 381
DB	359 DSQADVEMFRQDTVHHQESVE 379

RESULT 2

A34867
arrestin - fruit fly (*Drosophila melanogaster*)
C/Species: *Drosophila melanogaster*
C/Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 09-Jul-2004
R/Smith, D.P.; Shieh, B.H.; Zuker, C.S.
A/Title: Isolation and structure of an arrestin gene from *Drosophila*.
A/Reference number: A34867; MUID:90138925; PMID:1689056
A/Accession: A34867
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-364 <SMI>
R/Hyde, D.R.; Mecklenburg, K.L.; Pollock, J.A.; Vahnelic, T.S.; Benzer, S.
A/Title: Twenty *Drosophila* visual system cDNA clones: one is a homolog of human arrestin
A/Reference number: A34868; MUID:90138926; PMID:2105491
A/Accession: A34868
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-364 <HYD>
A/Cross-references: GB:M30140; NID:g156961; PIDN:AAA28380.1; PID:g156962
A/Genes: FLYBase:Arri
A/Cross-references: FLYBase:FBgn0000120
A/Introns: 36/3; 306/3; 349/3
C/Superfamily: arrestin

Query Match

Best Local Similarity 70.1%; Score 1384; DB 2; Length 364;
Matches 258; Conservative 51; Mismatches 54; Indels 4; Gaps 2;

QY 1 MVYNFKVKKCAPNGKVTLYMGKRDVHDVSGVEPIDGIIVLDDIYRDNKRVFGQIVCS 60
DB 1 MVYNFKVKKCAPNGKVTLYMGKRDVHDVSGVEPIDGIIVLDDIYRDNKRVFGQIVCS 60
QY 61 FRYGREDEVMGLNFOKELCLASEQIYPRPEKSDKEQTKLQERLLKLGSNAPFTFNIS 120
DB 61 FRYGREDEVMGLNFOKELCLASEQIYPRPEKSDKEQTKLQERLLKLGSNAPFTFNIS 120
QY 121 PNAPSSVTLOOGEDDNGPCGVSYVYKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGO 119
DB 120 PSSPASVVLQOKASDESQPCGVYFVKIFGTGSDCDRSHRSTVTLGIRKIQFAPTKQGO 119
QY 181 QPCTIVRKDFMLSPGELLEVTLDKQLYLHGERIGVNICIRNNSNKKVKKIKAMVQGV 179
DB 180 QPCTIVRKDFMLSPGELLEVTLDKQLYLHGERIGVNICIRNNSNKKVKKIKAMVQGV 179
QY 241 VVLFONGSRNTVASLETSEGCPIQPGSSLOKVMYLPPLSSNKKORRGIALDGOIKRQDQ 240
DB 240 VVLFONGSRNTVASLETSEGCPIQPGSSLOKVMYLPPLSSNKKORRGIALDGOIKRQDQ 239
QY 301 CLASTTLIAQPDQDAFGVYISYAVKVLFLGALGELSAELPFVLMHPKPGTKAKVITHA 299
DB 300 ALASTTLIASQDARDAFGIVSYAVKVLFLGALGELSAELPFVLMHPKPGTKAKVITHA 299
QY 361 DSQADVE 367
DB 357 EAEGSIE 363

RESULT 3

A55081
arrestin 1 - bluebottle fly (*Calliphora vicina*)
C/Species: *Calliphora vicina*
C/Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
R/Planger, A.; Malicki, D.; Whitney, M.; Paulsen, R.
A/Title: Mechanism of arrestin 2 function in rhabdomic photoreceptors.
A/Reference number: A55081; MUID:95014564; PMID:7929436

A/Accession: A55081

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-363 <PLA>

A/Cross-references: UNIPROT:P51486; GB:X79072; NID:g483527; PIDN:CAA55672.1; PID 94

A/Note: the source is designated as *Calliphora erythrocephala*

C/Superfamily: arrestin

Query Match

Best Local Similarity 67.7%; Score 1335; DB 2; Length 363;
Matches 248; Conservative 57; Mismatches 55; Indels 8; Gaps 2;

QY 1 MVYNFKVKKCAPNGKVTLYMGKRDVHDVSGVEPIDGIIVLDDIYRDNKRVFGQIVCS 60
DB 1 MVYNFKVKKCAPNGKVTLYMGKRDVHDVSGVEPIDGIIVLDDIYRDNKRVFGQIVCS 60
QY 61 FRYGREDEVMGLNFOKELCLASEQIYPRPEKSDKEQTKLQERLLKLGSNAPFTFNIS 120
DB 61 FRYGREDEVMGLNFOKELCLASEQIYPRPEKSDKEQTKLQERLLKLGSNAPFTFNIS 120
QY 121 PNAPSSVTLOOGEDDNGPCGVSYVYKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGO 119
DB 120 PSSPASVVLQOKASDESQPCGVYFVKIFGTGSDCDRSHRSTVTLGIRKIQFAPTKQGO 119
QY 181 QPCTIVRKDFMLSPGELLEVTLDKQLYLHGERIGVNICIRNNSNKKVKKIKAMVQGV 179
DB 180 QPCTIVRKDFMLSPGELLEVTLDKQLYLHGERIGVNICIRNNSNKKVKKIKAMVQGV 179
QY 241 VVLFONGSRNTVASLETSEGCPIQPGSSLOKVMYLPPLSSNKKORRGIALDGOIKRQDQ 240
DB 240 VVLFONGSRNTVASLETSEGCPIQPGSSLOKVMYLPPLSSNKKORRGIALDGOIKRQDQ 239
QY 301 CLASTTLIAQPDQDAFGVYISYAVKVLFLGALGELSAELPFVLMHPKPGTKAKVITHA 299
DB 300 SLASTTLIASQDARDAFGIVSYAVKVLFLGALGELSAELPFVLMHPKPGTKAKVITHA 299
QY 361 DSQADVE 368
DB 355 --QPEAET 360

RESULT 4

A56607
arrestin homolog - migratory locust
C/Species: *Locusta migratoria* (migratory locust)
C/Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 09-Jul-2004
R/Ramling, K.; Freitag, J.; Krieger, J.; Breer, H.
A/Title: Signal. 5, 69-80, 1993
A/Reference number: A56607; MUID:93199955; PMID:8452755
A/Contents: antennae
A/Accession: A56607
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-407 <RAM>
A/Cross-references: UNIPROT:P32122; GB:S57174; NID:g298755; PIDN:AAB25860.1; PID:g298756
A/Note: sequence extracted from NCBI backbone (NCBIN:127923, NCBI:P:127925)
C/Superfamily: arrestin

Query Match

Best Local Similarity 50.4%; Score 993.5; DB 2; Length 407;
Matches 202; Conservative 64; Mismatches 107; Indels 15; Gaps 8;

QY 6 KVFKKCAPNGKVTLYMGKRDVHDVSGVEPIDGIIVLDDIYRDNKRVFGQIVCSFRYGR 65
DB 14 KVFKKCAPNGKVTLYMGKRDVHDVSGVEPIDGIIVLDDIYRDNKRVFGQIVCSFRYGR 65
QY 66 EDEVMGLNFOKELCLASEQIYPRPEKSDKEQTKLQERLLKLGSNAPFTFNISPNAPS 125
DB 73 EDEVMGLNFOKELCLASEQIYPRPEKSDKEQTKLQERLLKLGSNAPFTFNISPNAPS 125
QY 126 SVTLQOGEDDNGPCGVSYVYKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGO-PCT 184

```

Db      132  S V T L Q P G D D D Q G K P L G V E Y S V K T V N G D H A E E K H K R S A V T L A I K L Q Y A P P T R G R L P S S      191
Qy      185  L V R K D F M L S P G E L E V T L D K O L Y L H G E R I G V N I C I R N S N K V Y K K I K A M V Q G V D V L F      244
Db      192  L V S K G F T F S G K I N L E V T L D R E I Y H G E K L A A N V I I N N S R K T Y K N I K V Y V Q H C E V T M V      251
Qy      245  Q N G S Y R N T V A S L E T S E G C P I Q P S S L Q K V M Y L T P L L S N K Q R R G T A L D G O I K R O D Q L A S      304
Db      252  - N A Q P S R H V A S L E T R E G C P I T P G A S F T K V F Y L V P C A A S N K D R I G T A L D G Y L K D D D V N L A S      310
Qy      305  T T L L A Q - P D Q R D A F G V I I S Y A V K Y K L F L G A L G S E L S A E L P F V L M H P K P G T - - - - K A K V I H      359
Db      311  S T I V S E G K N T T D A I G I V I S Y S L R V K Y L N C G T L G S E L Q T D V P F K L I H P A G T A E R E K A Q A I -      369
Qy      360  A D S Q A D V E T F R O D - - - - T I D Q A S V D F E      383
Db      370  - K K M K S I E R T R Y E N S C Y A A D D D D N I V F E      396

```

RESULT 5

arrestin homolog - fruit fly (*Drosophila miranda*)
C/Species: *Drosophila miranda*
C/Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C/Accession: S11566
R/Krishnan, R.; Ganguly, R.
Nucleic Acids Res. 18, 5894, 1990
A/Title: Nucleotide sequence of the arrestin-like 49 Kd protein gene of *Drosophila miranda*
A/Reference number: S11566; MUID:91016944; PMID:2216789
A/Accession: S11566
A/Status: preliminary; translation not shown
A/Molecule type: DNA
A/Residues: 1-401 <KRI>
A/Cross-references: UNIPROT:P19108; EMBL:X54084; NID:g7612; PIDN:CAA38019.1; PID:g2957339
C/Genetics:
A/Gene: FlyBase:Dm1r/Arr2
A/Cross-references: FlyBase:FBgn0012552
A/Introns: 286/1; 351/1
C/Superfamily: arrestin

Query Match	49.5%;	Score 977.5;	DB 2;	Length 401;
Best Local Similarity	48.5%;	Pred. No. 3.3e-70;		
Matches 190;	Conservative 76;	Mismatches 113;	Indels 13;	Gaps 6;

```
QY      1 MYVNFKVFKKCAPNGKVTLYMGKRDPVDHVSVEPIDGIVLVDXEYIRDNRRKVFQI VCS 60
      || : ||||| ||||| |::||::||: :::||::||: ||: |||||:: :
Db      1 MYVSVKVFKKATPNGKVTFYLGRRDFIDHLDYCDPVDGVIIVEPEYLK-NRKVFQGLATT 59
```

```
QY      61 FRYGDEDEVMGLNFQKELCLASEQLYVRPEKSDKEQTLOERLLKLTGSNAIPFTFNIS 120C
          :|||||||: ||||: ::|| |   : ||:::||:||||| ||||:
Db      60 YRYGDEDEVMGVKFESKELLISRDEIVEM-TNPMMENTPIQEKLVKLTGSNAHPFTTFHP 118C
```

[illegible]

```
QY      181 Q-PCTIVRKDFMLSPGELELEVTLDKQLYLHGERIGVNI CIRNNSNMKKVIKAMVQQGV 239
       : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      179 RLPSPLSVSKGFTFSNGKISLEVTLDRREIYYHGEKTAATAYOVSNSSKKSYSIKCFIVQHT 238
```

```

Qy      240 DVVLEFONGSYRNTVASIETSEGCPIQPGSSLQKWMYLLPLISSNKQRGIALDGOIKRQD 299
      :: : | : | | | | | | | | | | | | | | | | | | | | : :
Db      239 EITWV-NAQFSKHVAQIETKEGCPITPGANLTKTFYLLPLAANNKDRHGIALDGLHKDED 297

```

```

Qy      300 QCLASTTLLAQ-PDQRDAFGVIISYAVKKFLFLGALGGEISAELEPFLVLMHPKPGT----- 353
      |||::: : : ||::||:|:| | | | | : : | | |
Db      298 VNLASTMWQEGKNTGDACGIVISYVRKLNCGTLLGGEQOTDVPFKLLQDAPGTIEKKR 357

```

```

Qy      354 ---KAKVIHADSGADVETFRÖPTIDQASVDF 382
      355 | : : : | |
      356 SNAMKMKMSIEQHNRNVKGYQDDDDNIVFEDF 389
Db

```

RESULT 6
A34856
49K photoreceptor protein - fruit fly (*Drosophila melanogaster*)
C/Species: *Drosophila melanogaster*
C/Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 09-Jul-2004
C/Accession: A34856
R/Yamada, T.; Takeuchi, Y.; Komori, N.; Kobayashi, H.; Sakai, Y.; Hotta, Y.; Matsumoto, T.
Science 248, 483-485, 1990
A/Title: A 49-kilodalton phosphoprotein in the *Drosophila* photoreceptor is an arrestin homolog
A/Reference number: A34856; MUID:90232360; PMID:2158671
A/Accession: A34856
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-401 <YAM>
A/Cross-references: UNIPROT:P19107; GB:M32141; NID:g158157; PIDN:AAA28833.1; PID:g158158
C/Genetics:
A/Gene: FLYBase:Arr2
A/Cross-references: FLYBase:FBgn0000121
C/Superfamily: arrestin

Query Match
Best Local

Query Match	49.4%;	Score 975.5;	DB 2;	Length 401;
Best Local Similarity	48.5%;	Pred. No. 4.7e-70;		
Matches 190; Conservative	74;	Mismatches 115;	Indels 13;	Gaps 6;

```
QY      1 MYVNFKVFKKCAPNGKVTLVMGKRDPFVDHVSQVEPIDGVLLDDEYIRDNRKVFGLAVCS   60
       || : ||||| ||||| |:::||:|::: ::|||::|::: ::|||::|::: :
Db      1 MVSVKVFKKATPNGKVTFYLGRDFIHIDYCDDPVGDIVIVEPDYLR-NRKFVGQLATT    59
```

```
QY      61 FRYGREDEVMGLNFQKELCLASEQIYPRPEKSDKEOTKLQERLLKKLGSMNAPPTFNIS 120
        :|||||:| ||| ||| :| :||:|:||||:| |||:
Db      60 YRGRDEDEVMGVFSEKELICREQIVPM-TNPNMENPTMÖEKLVRKLGSSAHPPTFHFP 118
```

QY 121 PNASSVTLQOEGDDNDGDPGCVSYYVKIFAGESETDTRHRSTVTLGIKIKIQFAPTKQCG 180

Db 119 PNSSSVTLQOEGDDNGKPLGVEYETIRAFVGDSEDDQHKRSMVSLVTKLIQYAPLNRGQ 178

```
QY      181 Q-PCTLVVRKDFMUSPGELELEVLTLDKQYLHGERIGVNICIRNNSNKAKVKIKAMVOGV 239
          : : : | | | | : : | | | | : : | | | | : : |
Db      179 RLPSLSVSKGFTFSNGKISLEVTLDREIYYHGEXTATVQVSNNKS KSIKCFIVQHT 238
```

```
QY      240 DVVLFQNGSYRNTVASLETSEGCPIQFGSSLOKVMYLPBLLSSNKORRGIALDGOIKRQD 2999
      :: :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: |
Db      239 EITMV-NAQFSKHYAQLETKEGCPITPGANLTKTFYLIPLAANNKDKRHGIALDGHLKDED 2977
```

```
QY      300 QCTASTTLIAQ-PDQRDAFGVITISAVKVKLFLGALGSELSAELPFVLNHPKPQT----- 353
       |||::: | | :|| ::| | ||| : :|| | |
Db     298 VNLASSTMQEGKSITGDACGVIVISVRIKLNCGTIGGEMOTDVFPFKLIQPAPTIEKKR 357
```

```
QY      354 ---KAKVIHADSQADVETFRDITIDQASVDF 382
          | : : : | | |
Db      358 SNAMKKMKSTIEGHRNVKGYYDDDDDNIVFEDF 389
```

RESULT 7

arrestin 2 - bluebottle fly (*Calliphora vicina*)

C:\Date: 08-Jul-1995 #sequence revision 03-Aug-1995 #text change 09-Jul-2004

C;Accession: B55081; S44292

R;Planger, A.; Malicki, D.; Whitney, M.; Paulsen, R.

J. Biol. Chem. 269, 26969-26975, 1994

A;Title: Mechanism of arrestin 2 function in rhabdomic photoreceptors.

A;Reference number: A55081; MUID:95014564; PMID:7929436

A;Accession: B55081

A;Status: preliminary

A:molecule type: mRNA

A;Residues: 1-401 <PLA>

A; Cross-references: UNIPROT:P51487; EMBL:X79073; NID:g483583;

A;Note: the source is d

Query Match 47.8%; Score 942.5; DB 2; Length 401;

Best Local Similarity 47.7%; Pred. No. 2e-67;
Matches 187; Conservative 70; Mismatches 122; Indels 13; Gaps 6;

QY 1 MVTNFYFKKCAPNGKVTLYMGKRDVVDHVSVEPIIDGIVLDDDEYIRDNKRVFGQIVCS 6;
Db 1 MVTNFYFKKCAPNGKVTLYMGKRDVVDHVSVEPIIDGIVLDDDEYIRDNKRVFGQIVCS 60
QY 61 FRYGREDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKQERLLKLGSNALPFTFNIS 59
Db 60 YRYGREDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKQERLLKLGSNALPFTFNIS 120
QY 121 PNAPSSVTLLQOGEDNDGDPGCVSYVYKIFAGESETDRTHRSSTVTLGIRKIQAPTKOGQ 118
Db 119 PNAPSSVTLLQOGEDNDGDPGCVSYVYKIFAGESETDRTHRSSTVTLGIRKIQAPTKOGQ 180
QY 181 Q-PCTLVKDFMISPELEEVTLQKQYLHGERIGVNICIRNNSNMKVKIKAMVQOGV 178
Db 179 RLPSSLVSKGFTFSGNGKISLEVTLDREIYHGGKVAATVQVNNNSKKAIVNIKVFIIQHT 238
QY 240 DVVLFQNGSYRNTVASLETSEGCPIQFGSSLOKVMYLTPLSSNKQRGIALDGOIKRD 239
Db 239 EITMV-NAQFSKHVAQLETKEGCPTTPGAMLSKTFYLIPLASNNKDRHGIALDGHLOED 297
QY 300 QCLASTTLLAQ-PQORDAFGVIIISYAVKVLFLGALGELSAELPFVLMHPKPGT----- 297
Db 298 VNLASTMVQDGKSTGDACGIVISYVRIKLCNGCTLGGEIQTDPVFKLLQAPAGSVEKKR 353
QY 354 ---KAKVIHADSQADVETFRQDTIDQASVDF 382
Db 358 SNAMKKMKSIQHRNTKGYQDDDDNIVFEDF 389

RESULT 8

A34851
beta-arrestin, brain - bovine
C/Species: Bos primigenius taurus (cattle)
C/Date: 13-Jul-1990 #sequence_revision 21-Oct-1992 #text_change 09-Jul-2004
C/Accession: A34851; J02052
R/Lohse, M.J.; Benovic, J.L.; Codina, J.; Caron, M.G.; Lefkowitz, R.J.
A/Title: Beta-arrestin: a protein that regulates beta-adrenergic receptor function.
A/Reference number: A34851; PMID:90296080; PMID:21631110
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-418 <LOH>
A/Cross-references: UNIPROT:P17870; GB:M33601; NID:g162691; PIDN:AAA0387.1; PID:g162692
A/Experimental source: Brain
R/Sterne-Marr, R.; Gurevich, V.V.; Goldsmith, P.; Bodine, R.C.; Sanders, C.; Donoso, L.A.
J. Biol. Chem. 268, 15640-15648, 1993
A/Title: Polypeptide variants of beta-arrestin and arrestin3.
A/Reference number: A47140; PMID:93340166; PMID:8340388
A/Accession: J02052
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-15, 'C', '17-30, 'L', '32, 'K', '34-83, 'Y', '85-176, 'K', '178-206, 'L', '208-333, 342-418
A/Experimental source: lung, spleen
C/Comment: This protein is an arrestin homolog which acts analogously to desensitize the
F,1-418/Product: beta-arrestin, brain #status predicted <MAT>
F,1-333,342-418/Product: beta-arrestin, lung #status predicted <MA2>

Query Match

Best Local Similarity 45.8%; Score 903.5; DB 2; Length 418;
Matches 179; Conservative 76; Mismatches 112; Indels 13; Gaps 5;
QY 6 KVFKKCAPNGKVTLYMGKRDVVDHVSVEPIIDGIVLDDDEYIRDNKRVFGQIVCSFRYGR 65
Db 7 RVFKKASPNGKLTLYLGRKDFVDHIDLVEPVDGVLLVDPPEYLKE-RRVYVTLTCAFRYGR 65
QY 66 EEDVEMGLNFQKELCLASEQIYPRPEKSDKEQTKQERLLKLGSNALPFTFNISPNAPS 125
Db 66 EDLDVLTGLTFRKDLFVANVQSFPAPEDEKKPLTRLQERLLKLGSHAYPFTFPIPNLPC 125

QY 126 SVTLQOGEDNDGDPGCVSYVYKIFAGESETDRTHRSSTVTLGIRKIQAPTKOGQPCPTL 185
Db 126 SVTLQOGPEPDGKACGVYEVKAFCAENLEEKIHKNSVRLVIRKQVAPERPQPPTAE 185
QY 186 VRKDFMLSPGELEEVTLQKQYLHGERIGVNICIRNNSNMKVKIKAMVQOGVVDVLFQ 245
Db 186 TTRQFLMSKPLHLHSLDKEIYHGEPIISVNVHVTNNNTKTVKKIKISVQYADICLFN 245
QY 246 NGSYRNTVASLETSEGCPIQFGSSLOKVMYLTPLSSNKQRGIALDGOIKRDQCLAST 305
Db 246 TAQYKCPVAMEEADD--TVAPSTFCVKYTLTPFLANNRERKGLALDGLKHEDTNLASS 303
QY 306 TLADPDDQDAFGVIIISYAVKVLFL--GALGELSA-----ELPFVLMHPKPGTK--A 355
Db 304 TLREGANREILGIIVSYKVKLVVSRGGLGLDGLASSDVAVELPFTLMHPKKEEPHR 363
QY 356 KVIHADSQADVETFRQDTID 375
Db 364 EVPEHETPVDTNLIELDTND 383

RESULT 9

B43404
beta-arrestin1 - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C/Accession: B43404
R/Actramadal, H.; Arriza, J.L.; Aoki, C.; Dawson, T.M.; Codina, J.; Kwatra, M.M.; Snyder
J. Biol. Chem. 267, 17882-17890, 1992
A/Title: Beta-arrestin2, a novel member of the arrestin/beta-arrestin gene family.
A/Reference number: A43404; PMID:92388146; PMID:1517224
A/Accession: B43404
A/Status: Preliminary; not compared with conceptual translation
A/Molecule type: nucleic acid
A/Residues: 1-418 <ATT>
A/Cross-references: UNIPROT:P29066; GB:M91589; NID:g949985; PIDN:AAA74459.1; PID:g203102
C/Note: sequence extracted from NCBI backbone (NCBIF:112791)
C/Superfamily: arrestin

Query Match

Best Local Similarity 45.8%; Score 903.5; DB 2; Length 418;
Matches 178; Conservative 78; Mismatches 111; Indels 13; Gaps 5;
QY 6 KVFKKCAPNGKVTLYMGKRDVVDHVSVEPIIDGIVLDDDEYIRDNKRVFGQIVCSFRYGR 65
Db 7 RVFKKASPNGKLTLYLGRKDFVDHIDLVDVDPGVLLVDPPEYLKE-RRVYVTLTCAFRYGR 65
QY 66 EEDVEMGLNFQKELCLASEQIYPRPEKSDKEQTKQERLLKLGSNALPFTFNISPNAPS 125
Db 66 EDLDVLTGLTFRKDLFVANVQSFPAPEDEKKPLTRLQERLLKLGSHAYPFTFPIPNLPC 125
QY 126 SVTLQOGEDNDGDPGCVSYVYKIFAGESETDRTHRSSTVTLGIRKIQAPTKOGQPCPTL 185
Db 126 SVTLQOGPEPDGKACGVYEVKAFCAENLEEKIHKNSVRLVIRKQVAPERPQPPTAE 185
QY 186 VRKDFMLSPGELEEVTLQKQYLHGERIGVNICIRNNSNMKVKIKAMVQOGVVDVLFQ 245
Db 186 TTRQFLMSKPLHLHSLDKEIYHGEPIISVNVHVTNNNTKTVKKIKISVQYADICLFN 245
QY 246 NGSYRNTVASLETSEGCPIQFGSSLOKVMYLTPLSSNKQRGIALDGOIKRDQCLAST 305
Db 246 TAQYKCPVAMEEADD--TVAPSTFCVKYTLTPFLANNRERKGLALDGLKHEDTNLASS 303
QY 306 TLADPDDQDAFGVIIISYAVKVLFL--GALGELSA-----ELPFVLMHPKPGTK--A 355
Db 304 TLREGANREILGIIVSYKVKLVVSRGGLGLDGLASSDVAVELPFTLMHPKKEEPHR 363
QY 356 KVIHADSQADVETFRQDTID 375
Db 364 EVPEHETPVDTNLIELDTND 383

```
RESULT 10
B46682
beta-arrestin 1, splice form A - human
N:Contains: beta-arrestin 1, splice form B
C:Species: Homo sapiens (man)
C:Date: 22-Sep-1993 #sequence_revision 22-Sep-1993 #text_change 09-Jul-2004
C:Accession: B46682; A46682
R:Parutti, G.; Peracchia, F.; Sallese, M.; Ambrosini, G.; Masini, M.; Rotilio, D.; De Bi
J. Biol. Chem. 268, 9753-9761, 1993
A:Title: Molecular analysis of human beta-arrestin-1: cloning, tissue distribution, and
A:Reference number: A46682; MUID:93252853; PMID:8486659
A:Accession: B46682
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-418 <PAR1>
A:Cross-references: UNIPROT:P49407; GB:L04685; NID:g347956; PIDN:AAA35559.1; PID:g347958
A>Note: sequence extracted from NCBI backbone (NCBIP:134014)
A:Accession: A46682
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-333,342-418 <PAR2>
A:Cross-references: GB:L04685; NID:g347956; PIDN:AAA35556.1; PID:g347957
A>Note: sequence extracted from NCBI backbone (NCBIP:134015)
C:Genetics:
A:Gene: GDB:ARRB1; ARRI
A:Cross-references: GDB:141541; OMIM:107940
A:Map position: 11q13-11q13
C:Superfamily: arrestin
C:Keywords: alternative splicing
```

```
Query Match 45.2%; Score 891.5; DB 2; Length 418;
Best Local Similarity 46.3%; Pred. No. 2.5e-63;
Matches 176; Conservative 78; Mismatches 113; Indels 13; Gaps 5;

QY 6 KVFKKCAPNGKVTLYMGKRDVFDHVSQVEPIDGIVLDDIYIRDNRKVFQIVCSFRYGR 65
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 7 RVFKKASPNCKLTIVYLGKRDVFDHIDLVDVGVLDVDPYLYKE-RRVYVTLTCAFRYGR 65

QY 66 EEDVVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKLGSNAPFTFNISPNAPS 125
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 66 EDLDVLGLTFRKDLFVAVVQSPFPAPEDKPLTRLQERLLKLGSHAYPFTFEIPNLP 125

QY 126 SVTLQGGEDDNGDPCGVSYVVKIFAGESETDRTTHRSYVTLGIRKIQFAPTKQGQOPCTL 185
|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 126 SVTLQGGEDTGKACGVDEYAKAFCAENLEBKIHKNSVGLVIRKQYABERPGQPPTAE 185

QY 186 VRKDFMLSPGELELVTLDKQLYLHGERIGVNICIRNNSNGWVKIKAMVQGVVDVLFQ 245
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S18984
R:Rapoport, B.
submitted to the EMBL Data Library, November 1991
A:Description: Isolation of a novel cDNA belonging to the arrestin family from human thy.
A:Reference number: S18984
A:Accession: S18984
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-409 <RAP>
A:Cross-references: UNIPROT:P32121; EMBL:Z11501; NID:g28850; PIDN:CAA77577.1; PID:g28851
C:Superfamily: arrestin

Db 364 EVPENETPVDTNLIELDTND 383
```

```
RESULT 11
A47140
arrestin arr3L - bovine
N:Contains: arrestin arr3S
C:Species: Bos primigenius taurus (cattle)
C:Date: 16-Feb-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: A47140; B47140; J02051
R:Stearns-Marx, R.; Gurevich, V.V.; Goldsmith, P.; Bodine, R.C.; Sanders, C.; Donoso, L.A
J. Biol. Chem. 268, 15640-15648, 1993
A:Title: Polypeptide variants of beta-arrestin and arrestin3.
```

```
A:Reference number: A47140; MUID:93340166; PMID:8340388
A:Accession: A47140
A:Molecule type: mRNA
A:Residues: 1-420 <STE>
A:Cross-references: UNIPROT:P32120; GB:L14641
A:Experimental source: brain
A>Note: sequence extracted from NCBI backbone (NCBIN:136006, NCBIP:136007)
A:Accession: B47140
A:Molecule type: mRNA
A:Residues: 1-362,374-420 <ST2>
C:Comment: This protein plays a role in the regulation of G-protein-coupled receptors.
C:Superfamily: arrestin
F:1-420/Product: arrestin arr3L #status predicted <MAT>
F:1-362,374-420/Product: arrestin arr3S #status predicted <MA2>
```

```
Query Match 45.0%; Score 887; DB 2; Length 420;
Best Local Similarity 48.3%; Pred. No. 5.8e-63;
Matches 167; Conservative 78; Mismatches 97; Indels 4; Gaps 3;

QY 6 KVFKKCAPNGKVTLYMGKRDVFDHVSQVEPIDGIVLDDIYIRDNRKVFQIVCSFRYGR 65
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 8 RVFKKSPNCKLTIVYLGKRDVFDHLDKVDVGVLDVDPYLYKD-RKVYVTLTCAFRYGR 66

QY 66 EEDVVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKLGSNAPFTFNISPNAPS 125
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 67 EDLDVLGLSFRKDLFIANYQAFPPTPNRPPTRLQERLLKLGQHAHPFFFTIPQNLPC 126

QY 126 SVTLQGGEDDNGDPCGVSYVVKIFAGESETDRTTHRSYVTLGIRKIQFAPTKQGQOPCTL 185
|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 127 SVTLQGGEDTGKACGVDFEIRAFCAKSLBEKSHKNSVRLVIRKQVAFBEKPGQPSAB 186

QY 186 VRKDFMLSPGELELVTLDKQLYLHGERIGVNICIRNNSNGWVKIKAMVQGVVDVLFQ 245
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 187 TTRHFLMSDRSLHLLEASLDKELYYHGEPLNVNVTNNGTKTVKKIKVSRQYADICLFS 246

QY 246 NSYRNTVASLETSEGCPIQPGSSLOQVWYLTPLLSNKGORGIALDQAIKRDQCLAST 305
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 247 TAQYKCPVAQVEQDD-QVSPSSSTFCVKYTTITPLLSNNEKRGIALDGKLGHEDTNLASS 304

QY 306 TLLAQPDQRDAFGVIISYAVKVLFLGALGELSABLPEVLMHPKP 351
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 305 TIVKEGANKEVLGILVSRYKVKLV-SRGGDVSVLELPEVLMHPKP 349
```

```
RESULT 12
S18984
arrestin - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S18984
R:Rapoport, B.
submitted to the EMBL Data Library, November 1991
A:Description: Isolation of a novel cDNA belonging to the arrestin family from human thy.
A:Reference number: S18984
A:Accession: S18984
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-409 <RAP>
A:Cross-references: UNIPROT:P32121; EMBL:Z11501; NID:g28850; PIDN:CAA77577.1; PID:g28851
C:Superfamily: arrestin
```

```
Query Match 44.7%; Score 882; DB 2; Length 409;
Best Local Similarity 48.3%; Pred. No. 1.4e-62;
Matches 167; Conservative 76; Mismatches 99; Indels 4; Gaps 3;

QY 6 KVFKKCAPNGKVTLYMGKRDVFDHVSQVEPIDGIVLDDIYIRDNRKVFQIVCSFRYGR 65
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 8 RVFKKSPNCKLTIVYLGKRDVFDHLDKVDVGVLDVDPYLYKD-RKVYVTLTCAFRYGR 66

QY 66 EEDVVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKLGSNAPFTFNISPNAPS 125
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 67 EDLDVLGLSFRKDLFIATYQAFPVPVNPBPPTRLQDRLLRLKLGQHAHPFFFTIPQNLPC 126
```


This Page Blank (uspto)

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 9, 2005, 23:23:51 ; Search time 64 Seconds
(without alignments)
3064.474 Million cell updates/sec

Title: US-10-056-405-2
Perfect score: 1973
Sequence: 1 MVYNFKVFKKCAPNGKVTLY.....ADVETFRQDTIDQASVDFE 383

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03:*
1: uniProt_sprot:*
2: uniProt_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1973	100.0	383	2 Q95NPF3	Q95NPF3 anopheles g
2	1973	100.0	417	2 Q7PMG5	Q7PMG5 anopheles g
3	1515	76.8	381	2 Q9BIG9	Q9BIG9 ascalaphus
4	1499	76.0	381	1 ARRH_HELVI	P55274 heliothis v
5	1384	70.1	364	1 ARRA_DROME	P15372 drosophila
6	1335	67.7	363	1 ARRA_CALVI	P51486 calliphora
7	1254	63.6	245	2 Q6VPP0	Q6VPP0 anopheles g
8	1036	52.5	431	2 Q7Q2V9	Q7Q2V9 anopheles g
9	1023	51.8	398	2 Q66GU6	Q66GU6 anopheles g
10	1023	51.8	401	2 Q7Q5Q8	Q7Q5Q8 anopheles g
11	1002	50.8	470	2 Q9V393	Q9V393 drosophila
12	993.5	50.4	407	1 ARRH_LOCM1	P32122 locusta mig
13	982.5	49.8	401	1 ARRB_DROME	P19107 drosophila
14	977.5	49.5	401	1 ARRB_DROME	P19108 drosophila
15	937.5	47.5	400	1 ARRB_CALVI	P51487 calliphora
16	931	47.2	400	1 ARRH_LIMPO	P51484 limulus pol
17	931	47.2	419	2 Q86BW6	Q86BW6 halocynthia
18	922.5	46.8	418	2 Q8MYB1	Q8MYB1 ciona intes
19	919	46.6	412	2 Q64ID8	Q64ID8 xenopus lae
20	912.5	46.2	410	2 Q8BTJ5	Q8BTJ5 mus musculu
21	904.5	45.8	418	2 Q8BWG8	Q8BWG8 mus musculu
22	903.5	45.8	418	1 ARRI_BOVIN	P29066 ratu
23	903.5	45.8	418	1 ARRI_BOVIN	P29066 ratu
24	900.5	45.6	418	1 ARRI_HUMAN	P49407 homo sapien
25	893	45.3	408	2 Q7T2D2	Q7T2D2 brachydanio
26	888.5	45.0	435	1 ARRB_CAEBL	P51485 caenorhabd1
27	887	45.0	420	1 ARR2_BOVIN	P32120 bos tauru
28	885	44.9	409	1 ARR2_HUMAN	P32121 homo sapien
29	881	44.7	409	2 Q6ICT3	Q6ICT3 homo sapien
30	880.5	44.6	410	1 ARRI_RABIT	Q95223 oryctolagus
31	880	44.6	408	2 Q6DFC4	Q6DFC4 xenopus lae

32	878.5	44.5	406	2 Q6PEK2	Q6PEK2 brachydanio
33	876	44.4	408	2 Q6GPY2	Q6GPY2 xenopus lae
34	871	44.1	407	1 ARRI_ONCMY	P51466 oncorhynchu
35	869.5	44.1	410	1 ARR2_MOUSE	Q91Y14 mus musculu
36	869.5	44.1	410	1 ARR2_RAT	P29067 ratu
37	863	43.7	405	1 ARR3_ONCMY	P51468 oncorhynchu
38	861	43.6	405	1 ARR2_ONCMY	P51467 oncorhynchu
39	853	43.2	392	2 Q9PTB7	Q9PTB7 ambystoma t
40	810	41.1	387	1 ARRC_XENLA	P51483 xenopus lae
41	791	40.1	392	2 Q6NUV2	Q6nuv2 brachydanio
42	785.5	39.8	389	1 ARRC_RANCA	P51481 rana catgeb
43	784.5	39.8	389	1 ARRC_RANPI	P51482 rana pipien
44	783.5	39.7	403	1 ARRS_MOUSE	P20443 mus musculu
45	781.5	39.6	403	1 ARRS_RAT	P15887 ratu

ALIGNMENTS

RESULT 1					
ID	Q95NPF3	PRELIMINARY;	PRT;	383 AA.	
AC	Q95NPF3;				
DT	01-DEC-2001 (Tremblrel. 19, Created)				
DT	01-DEC-2001 (Tremblrel. 19, Last sequence update)				
DT	05-JUL-2004 (Tremblrel. 27, Last annotation update)				
DE	Arrestin.				
GN	Name=Arri1;				
OS	Anopheles gambiae (African malaria mosquito).				
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;				
OC	Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.				
OX	NCBI_Taxid=7165;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Antennae, and Head;				
RX	MEDLINE=21680430; PubMed=11822731;				
RA	Ricci I., Santolamazza F., Costantini C., Pavia G.;				
RT	"Molecular characterization and chromosomal mapping of transcripts				
RT	having tissue-specific expression in the malaria mosquito anopheles				
RT	gambiae: possible involvement in visual or olfactory processes.";				
RL	Parasitol. Res. 88:1-8(2002).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=G3;				
RX	MEDLINE=21819361; PubMed=11792843; DOI=10.1073/pnas.022505499;				
RA	Merrill C.E., Riesgo-Escovar J., Pitts R.J., Kafatos F.C.;				
RA	Carlson J.R., Zweibel L.J.;				
RT	"Visual arrestin in olfactory pathways of Drosophila and the malaria				
RT	vector mosquito Anopheles gambiae.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 99:1633-1638(2002).				
DR	EMBL; AJ04409; CAC39103.2; -.				
DR	EMBL; AY017417; AAG54081.1; -.				
DR	HSSP; P17870; 1G4M.				
DR	GO; GO:0007600; P:sensory perception; IEA.				
DR	GO; GO:0007165; P:signal transduction; IEA.				
DR	InterPro; IPR000698; Arrestin.				
DR	InterPro; IPR011022; Arrestin_C.				
DR	InterPro; IPR011021; Arrestin_N.				
DR	Pfam; PF02752; Arrestin_C; 1.				
DR	Pfam; PF00339; Arrestin_N; 1.				
DR	PRINTS; PR00309; ARRESTIN.				
DR	PROSITE; PS00295; ARRESTINS; 1.				
SQ	SEQUENCE 383 AA; 42809 MW; FA946438592BBS3E CRC64;				
Query Match 100.0%; Score 1973; DB 2; Length 383;					
Best Local Similarity 100.0%; Pred. No. 1.1e-144;					
Matches 383, Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1 MVYNFKVFKKCAPNGKVTLYMGKDFVHVSQVEPIDGIWLDDEYIRDNKVFQIYVCS 60				
DB	1 MVYNFKVFKKCAPNGKVTLYMGKDFVHVSQVEPIDGIWLDDEYIRDNKVFQIYVCS 60				
QY	61 FRYGREDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKLGSNAPPTFNIS 120				

Db 61 FRYGREDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLOERLLKKGLSNAIPFTFNIS 120
QY 121 PNPASSVTLLQGGEDDNGDPCGVSYYVKIFAGESETDTRHRSSTVTLGIRKIQFAPTKOG 180
Db 121 PNPASSVTLLQGGEDDNGDPCGVSYYVKIFAGESETDTRHRSSTVTLGIRKIQFAPTKOG 180
QY 181 QPCTLVKRD FMLS PGELELEVTLDKQLYLHGERIGVNICIRNNSNMKVKKIKAMVQOGVD 240
Db 181 QPCTLVKRD FMLS PGELELEVTLDKQLYLHGERIGVNICIRNNSNMKVKKIKAMVQOGVD 240
QY 241 VVLFQNGSYRNTVASLETSEGCPIQPGSSLOKVMYLTPLSSNKQRGIALDGOIKRQDQ 300
Db 241 VVLFQNGSYRNTVASLETSEGCPIQPGSSLOKVMYLTPLSSNKQRGIALDGOIKRQDQ 300
QY 301 CLASTTLLAQPDPQDAFGVITISYAVKVLFLGALGELSAELPFVLMHPKPGTKAKVIHA 360
Db 301 CLASTTLLAQPDPQDAFGVITISYAVKVLFLGALGELSAELPFVLMHPKPGTKAKVIHA 360
QY 361 DSQADVETFRQDITIDQASVDPE 383
Db 361 DSQADVETFRQDITIDQASVDPE 383

RESULT 2

07PMG5
ID 07PMG5 PRELIMINARY; PRT; 417 AA.
AC 07PMG5;
DT 01-MAR-2004 (Tremblrel. 26, Created)
DT 01-MAR-2004 (Tremblrel. 26, Last sequence update)
DE ENSANGP0000012569 (Fragment).
GN Name=ENSANG0000010080;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR HSSP; AAAB01008980; EAA13874.2; --
DR GO; GO:0007600; P:sensory perception, IEA.
DR GO; GO:0007165; P:signal transduction, IEA.
DR InterPro; IPR000698; Arrestin.
DR InterPro; IPR011022; Arrestin.
DR InterPro; IPR011021; Arrestin_C.
DR Pfam; PF02752; Arrestin_N.
DR Pfam; PF00339; Arrestin_C; 1.
DR PRINTS; PR00309; ARRESTIN.
DR PRODOM; PD002099; ARRESTIN.
DR PROSITE; PS00295; ARRESTIN; 2.
FT NON TER
SQ SEQUENCE 417 AA; 46591 MW; 4EE98A3C32257FC0 CRC64;

Query Match
Best Local Similarity 100.0%; Score 1973; DB 2; Length 417;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVYNFKVFKKCAPNGKVTLYMGRDVFVHSGVEPIDGIVLDDIYIRDNKRVGOIVCS 60
Db 35 MVYNFKVFKKCAPNGKVTLYMGRDVFVHSGVEPIDGIVLDDIYIRDNKRVGOIVCS 60
QY 61 FRYGREDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLOERLLKKGLSNAIPFTFNIS 120
Db 95 FRYGREDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLOERLLKKGLSNAIPFTFNIS 120
QY 121 PNPASSVTLLQGGEDDNGDPCGVSYYVKIFAGESETDTRHRSSTVTLGIRKIQFAPTKOG 180

Db 155 PNPASSVTLLQGGEDDNGDPCGVSYYVKIFAGESETDTRHRSSTVTLGIRKIQFAPTKOG 214
QY 181 QPCTLVKRD FMLS PGELELEVTLDKQLYLHGERIGVNICIRNNSNMKVKKIKAMVQOGVD 240
Db 215 QPCTLVKRD FMLS PGELELEVTLDKQLYLHGERIGVNICIRNNSNMKVKKIKAMVQOGVD 240
QY 241 VVLFQNGSYRNTVASLETSEGCPIQPGSSLOKVMYLTPLSSNKQRGIALDGOIKRQDQ 300
Db 275 VVLFQNGSYRNTVASLETSEGCPIQPGSSLOKVMYLTPLSSNKQRGIALDGOIKRQDQ 300
QY 301 CLASTTLLAQPDPQDAFGVITISYAVKVLFLGALGELSAELPFVLMHPKPGTKAKVIHA 360
Db 335 CLASTTLLAQPDPQDAFGVITISYAVKVLFLGALGELSAELPFVLMHPKPGTKAKVIHA 360
QY 361 DSQADVETFRQDITIDQASVDPE 383
Db 395 DSQADVETFRQDITIDQASVDPE 417

RESULT 3

09BIG9
ID 09BIG9 PRELIMINARY; PRT; 381 AA.
AC 09BIG9;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DE Arrestin.
GN Name=sarl;
OS Ascalaphus macaronius.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Neuroptera; Ascalaphidae; Ascalaphus.
OX NCBI_TaxID=146496;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Head;
RX MEDLINE=21184354; PubMed=11287006; DOI=10.1016/S0014-5793(01)02287-6;
RT "UV-light-dependent binding of a visual arrestin 1 isoform to
RT photoreceptor membranes in a neuropteran (Ascalaphus) compound eye."
RL FRBS Lett. 493:112-116(2001).
DR EMBL; AJ303080; CAC36938.1; --
DR HSSP; P17870; 1G4M.
DR GO; GO:0007600; P:sensory perception, IEA.
DR GO; GO:0007165; P:signal transduction, IEA.
DR InterPro; IPR000698; Arrestin.
DR InterPro; IPR011022; Arrestin.
DR InterPro; IPR011021; Arrestin_C.
DR Pfam; PF02752; Arrestin_N.
DR Pfam; PF00339; Arrestin_C; 1.
DR PRINTS; PR00309; ARRESTIN.
DR PROSITE; PS00295; ARRESTIN; 1.
SQ SEQUENCE 381 AA; 42789 MW; 451DEF465969857D CRC64;

Query Match
Best Local Similarity 76.8%; Score 1515; DB 2; Length 381;
Matches 289; Conservative 46; Mismatches 41; Indels 6; Gaps 4;
QY 1 MVYNFKVFKKCAPNGKVTLYMGRDVFVHSGVEPIDGIVLDDIYIRDNKRVGOIVCS 59
Db 1 MVANFKVFKKSSPNKRTIYLGKRFVDVHSGVEPIDGIVLDDIYIRDNKRVGOIVCS 59
QY 60 SFRYGREDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLOERLLKKGLSNAIPFTFNIS 119
Db 61 SFRYGREDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLOERLLKKGLSNAIPFTFNIS 119
QY 120 SPNPASSVTLLQGGEDDNGDPCGVSYYVKIFAGESETDTRHRSSTVTLGIRKIQFAPTKOG 178
Db 119 SPNPASSVTLLQGGEDDNGDPCGVSYYVKIFAGESETDTRHRSSTVTLGIRKIQFAPTKOG 178
QY 180 QPCTLVKRD FMLS PGELELEVTLDKQLYLHGERIGVNICIRNNSNMKVKKIKAMVQOGV 239
Db 179 QPCTLVKRD FMLS PGELELEVTLDKQLYLHGERIGVNICIRNNSNMKVKKIKAMVQOGV 239

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195 (2000).
 RN [4]
 RP GENOME REANNOTATION.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochownik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celisner S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.,
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley; TISSUE=Head;
 RX MEDLINE=22426066; PubMed=12537569;
 RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
 RA George R.A., Guarin H., Krommiller B., Pacleb J.M., Park S., Wan K.H.,
 RA Rubin G.M., Celisner S.E.,
 RT "A *Drosophila* full-length cDNA resource.";
 RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
 RN [6]
 RP PHOSPHORYLATION.
 RX MEDLINE=91282780; PubMed=1905538;
 RA Matsumoto H., Yamada T.,
 RT "Phosphatase I and II: arrestin homologs which undergo differential
 RT light-induced phosphorylation in the *Drosophila* photoreceptor in
 RL vivo.";
 RL Biochem. Biophys. Res. Commun. 177:1306-1312(1991).
 RN [7]
 RP FUNCTION.
 RX MEDLINE=93303590; PubMed=8316831;
 RA Dolph P.J., Ranganathan R., Colley N.J., Hardy R.W., Socolich M.,
 RA Zuker C.S.,
 RT "Arrestin function in inactivation of G protein-coupled receptor
 RT rhodopsin in vivo.";
 RL Science 260:1910-1916(1993).
 CC -1- FUNCTION: Regulates photoreceptor cell deactivation. Arr1 and Arr2
 CC for the termination of the phototransduction cascade.
 CC -1- TISSUE SPECIFICITY: Expressed specifically and abundantly in the
 CC photoreceptors. Inner and outer segments, and the inner plexiform
 CC -1- PTM: Phosphorylated, but does not undergo light-induced
 CC phosphorylation.
 CC -1- SIMILARITY: Belongs to the arrestin family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M30177; -; NOT_ANNOTATED_CDS.
 DR EMBL; M30140; AAA28380.1; -;
 DR EMBL; AEO03657; AAF53644.1; -;
 DR EMBL; AY061824; AAL27635.1; -;
 DR PIR; A34867; A34867.
 DR HSSP; P17870; 1G4M.
 DR IntAct; P15372; -;
 DR FlyBase; FBgn0000120; Arr1.
 DR GO; GO:0005624; C:membrane fraction; IDA.
 DR GO; GO:0016028; C:membrane fraction; IDA.
 DR GO; GO:0016060; P:metarhodopsin inactivation; IGI.
 DR InterPro; IPR000698; Arrestin.
 DR InterPro; IPR011022; Arrestin_C.

DR InterPro; IPR011021; Arrestin_N.
 DR Pfam; PF02752; Arrestin_C_1.
 DR Pfam; PF00339; Arrestin_N_1.
 DR PRINTS; PR00309; ARRESTIN.
 DR ProDom; PD002099; ARRESTIN.
 DR PROSITE; PS00295; ARRESTIN; 2.
 KW phosphorylation; sensory transduction; vision.
 SQ SEQUENCE 364 AA; 40771 MW; 0DCC764C4F890FC2 CRC64;
 Query Match 70.1%; Score 1384; DB 1; Length 364;
 Best Local Similarity 70.3%; Pred. No. 5.1e-99;
 Matches 258; Conservative 51; Mismatches 54; Indels 4; Gaps 2;
 QY 1 MVTNFKVKKCAPNGKVTLYMGKDFVDHVSQVEPIDGIVLDDDEYIRDNKRVGQIVCS 60
 DB 1 MVTNFKVKKCAPNGKVTLYMGKDFVDHVSQVEPIDGIVLDDDEYIRDNKRVGQIVCS 60
 QY 61 FRYGREDEVMGLNFOKELCLASQIYPREKSDKEQTKLQERLKLGSNAIPFTNIS 120
 DB 61 FRYGREDEVMGLNFOKELCLASQIYPREKSDKEQTKLQERLKLGSNAIPFTNIS 120
 QY 121 PNAPSVTLQGGEDNDGDCVSVYVYKIFAGESETRDRTRSTVTLGIRKIQFAPTKQ 119
 DB 121 PNAPSVTLQGGEDNDGDCVSVYVYKIFAGESETRDRTRSTVTLGIRKIQFAPTKQ 119
 QY 120 PSSPASVTLQKASDESQCGVQYFVKIFGDSDCDRSHRSTINIGIRKQVAPTKQGI 180
 DB 120 PSSPASVTLQKASDESQCGVQYFVKIFGDSDCDRSHRSTINIGIRKQVAPTKQGI 180
 QY 181 QPCTLVKRDMLSPGELELVTLQKLYLNGERIGVNICIRNSNKKVKKIKAMVQGV 179
 DB 181 QPCTLVKRDMLSPGELELVTLQKLYLNGERIGVNICIRNSNKKVKKIKAMVQGV 179
 QY 180 QPCTLVKRDMLSPGELELVTLQKLYLNGERIGVNICIRNSNKKVKKIKAMVQGV 240
 DB 180 QPCTLVKRDMLSPGELELVTLQKLYLNGERIGVNICIRNSNKKVKKIKAMVQGV 240
 QY 241 VVLFONGSYRNTVASLETSEGPISQKVMYLTPLSSNKKRGIADGQIKQDQ 239
 DB 241 VVLFONGSYRNTVASLETSEGPISQKVMYLTPLSSNKKRGIADGQIKQDQ 239
 QY 240 VVLFONGSYRNTVASLETSEGPISQKVMYLTPLSSNKKRGIADGQIKQDQ 300
 DB 240 VVLFONGSYRNTVASLETSEGPISQKVMYLTPLSSNKKRGIADGQIKQDQ 300
 QY 301 CLASTTLAQPORDAFGIYISYAVKVLFLGALGGEISAEPLFVLMHPKPGTRAKVIHA 299
 DB 301 CLASTTLAQPORDAFGIYISYAVKVLFLGALGGEISAEPLFVLMHPKPGTRAKVIHA 299
 QY 300 ALASTTLISQDARDAGIIVSYAVKVLFLGALGGEISAEPLFVLMHPKPGTRAKVIHA 360
 DB 300 ALASTTLISQDARDAGIIVSYAVKVLFLGALGGEISAEPLFVLMHPKPGTRAKVIHA 360
 QY 361 DQADAVE 367
 DB 361 DQADAVE 367
 QY 357 EAEGSIE 363
 DB 357 EAEGSIE 363

RESULT 6
 ARR1_CALVI
 ID ARR1_CALVI STANDARD; PRT; 363 AA.
 AC PS1486;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Phosrestin II (Arrestin A) (Arrestin 1).
 GN Name=ARR1;
 OS Calliphora vicina (Blue blowfly) (Calliphora erythrocephala).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Calliphoridae; Calliphora.
 OC NCBI_TaxID=7373;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Retina;
 RX MEDLINE=95014564; PubMed=7929436;
 RA Planger A., Malicki D., Whitney M., Paulsen R.,
 RT "Mechanism of arrestin 2 function in rhodomeric photoreceptors.";
 RL J. Biol. Chem. 269:26969-26975(1994).
 CC -1- SIMILARITY: Belongs to the arrestin family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; X79072; CAA55672.1; -.
DR PIR; A55081; A55081.
DR HSSP; P17870; 1G4M.
DR InterPro; IPR00698; Arrestin.
DR InterPro; IPR011022; Arrestin_C.
DR InterPro; IPR011021; Arrestin_N.
DR Pfam; PF02752; Arrestin_C; 1.
DR Pfam; PF00339; Arrestin_N; 1.
DR PRINTS; PR00309; ARRESTIN.
DR ProDom; PD002099; Arrestin; 2.
DR PROSITE; PS00295; ARRESTINS; 1.
KW Sensory transduction; Vision.
SQ SEQUENCE 363 AA; 40680 MW; 7C345D818E46C23E CRC64;

Query Match 67.7%; Score 1335; DB 1; Length 363;
Best Local Similarity 67.4%; Pred. No. 3.2e-95;
Matches 248; Conservative 57; Mismatches 55; Indels 8; Gaps 2;

QY 1 MYYNFKVFKKCAPNGKVTLYMGKRDVVDHVSVEPIDGIVVLDDEYIRDNKRVFGQIVCS 60
DB 1 MYYNFKIIFKASPNMMVTLYMNRREFVDSVTQVEPVDGIVVLDDEYIRDNKRIFFVQLICN 60
QY 61 FRYGREDEVMGLNFQKELCLASEQIYPRPEKSKDEQTLQERLLKLGSSNAIPFTFNIS 120
DB 61 FRYGREDEMIIGLRFQKELILVSQPVYFE-QKIDILTKMQERLLKLGSSNAYPFILEMP 119
QY 121 PNAPSSVTLQQGEDNGDPCGVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQG 180
DB 120 PSSPASVVLQQKANDSTQPCGVQFVKYFAGENDCDRSHRSTVNLGIRKVQYAPTGTGI 179
QY 181 QPCTLVKRDPMLSPELELEVTLDKQLYHGERIGVNICIRNSNKMVKIKAMVQGV 240
DB 180 QPCTLVKRDPLSPGELELEVTLDKQLYHGEKISINICVNNNSNMVKIKAMVQGV 239
QY 241 VVLFQNGSYRNTVASLETSEGCPIQPGSSLQKMYLTPLISSNKORRGIALDGQIKRQD 300
DB 240 VVLFQNGQFRNTIAFAESSEGCPLNPGSSLQKIMYLVPMIAANCDRAGIAVEGDVKHKNT 299
QY 301 CLASTTLAQPDQDAFGVIISYAVKVLFLGALGSELAEPLFVLMHPKGTAKAVIHA 360
DB 300 SLASTTLASQEARDAFGIVSYAVKVLFLGALGSELAEPLFILMHPKSLKA----- 354
QY 361 DSQADVERT 368
DB 355 --QPEAET 360

RESULT 7

Q6VPP0 PRELIMINARY; PRT; 245 AA.
AC Q6VPP0;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Arrestin (Fragment).
OS Anopheles gambiae (African malaria mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=7165;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=4aR, Yaounde, and L3-5;
RA Morlais I., Poncon N., Simard F., Cohuet A., Fontenille D.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY333991; AAR01116.1; -.
DR EMBL; AY333992; AAR01117.1; -.
DR EMBL; AY333993; AAR01118.1; -.
DR EMBL; AY333995; AAR01120.1; -.
DR EMBL; AY333990; AAR01115.1; -.
DR EMBL; AY333996; AAR01121.1; -.
DR EMBL; AY333994; AAR01119.1; -.
DR HSSP; P08168; 1AYR.
DR GO; GO:0007600; P:sensory perception; IEA.

DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR00698; Arrestin.
DR InterPro; IPR011022; Arrestin_C.
DR InterPro; IPR011021; Arrestin_N.
DR Pfam; PF02752; Arrestin_C; 1.
DR Pfam; PF00339; Arrestin_N; 1.
DR PRINTS; PR00309; ARRESTIN.
DR ProDom; PD002099; Arrestin; 2.
FT NON_TER 1 1
FT NON_TER 245 245
SQ SEQUENCE 245 AA; 27038 MW; 86D8F4520115DA5F CRC64;

Query Match 63.6%; Score 1254; DB 2; Length 245;
Best Local Similarity 100.0%; Pred. No. 3.7e-89;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 LQQGEDNGDPCGVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKGQGPCTLVRK 188
DB 1 LQQGEDNGDPCGVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKGQGPCTLVRK 60
QY 189 DFMLSPGELELEVTLDKQLYHGERIGVNICIRNSNKMVKIKAMVQGV 248
DB 61 DFMLSPGELELEVTLDKQLYHGERIGVNICIRNSNKMVKIKAMVQGV 120
QY 249 YRNTVASLETSEGCPIQPGSSLQKMYLTPLISSNKORRGIALDGQIKRQDCLASTTL 308
DB 121 YRNTVASLETSEGCPIQPGSSLQKMYLTPLISSNKORRGIALDGQIKRQDCLASTTL 180
QY 309 AQPDDQDAFGVIISYAVKVLFLGALGSELAEPLFVLMHPKGTAKAVIHADSQADVERT 368
DB 181 AQPDDQDAFGVIISYAVKVLFLGALGSELAEPLFVLMHPKGTAKAVIHADSQADVERT 240
QY 369 FRQDT 373
DB 241 FRQDT 245

RESULT 8

Q7Q2V9 PRELIMINARY; PRT; 431 AA.
AC Q7Q2V9;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Ebip4989 (Kurtz arrestin-like protein Ark) (Fragment).
GN Name=ebip4989; Synonyms=ARRK; ORFNames=ENSANGG0000003863;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RX MEDLINE=23159591; PubMed=14986925;
RA Merrill C.E., Pitts R.J., Zwiebel L.J.;
RT "Molecular characterization of arrestin family members in the malaria vector mosquito, Anopheles gambiae.";
RL Insect Mol. Biol. 12:641-650(2003).
CC -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.
DR EMBL; AAB01008966; EAA13078.1; -.
DR EMBL; BK000997; DAA00889.1; -.
DR HSSP; P17870; 1G4M.
DR GO; GO:0007600; P:sensory perception; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR00698; Arrestin.
DR InterPro; IPR011022; Arrestin_C.

DR InterPro; IPR011021; Arrestin_N.
DR Pfam; PF02752; Arrestin_C; 1.
DR PRINTS; PR00309; Arrestin_N; 1.
DR PRODOM; PD002099; Arrestin_N; 1.
DR PROSITE; PS00295; Arrestin; 2.
FT NON_TER 1
FT 431 431
SQ SEQUENCE 431 AA; 47810 MW; 85C110785A815916 CRC64;

Query Match
Best Local Similarity 52.5%; Score 1036; DB 2; Length 431;
Matches 191; Conservative 75; Mismatches 85; Indels 2; Gaps 2;

QY 6 KVFKKCAPNGKVTLYMGKRDVDSGVPEPIDGIVLDDERYTRDNKRVGQIVCSFRYGR 65
DB 7 RVFKKSSNGKITVYLGKRDVDFHITHVDPIDGVVLDIDPDYKE-RKVFGLHAFRYGR 65
QY 66 EEDVWGLNFOKELCLASEQIYPRPEKSDKEQTKLOERLKLGSNAIPFTFNISPNAPS 125
DB 66 EDLDVLTGLTRKDLVYLASEQIYPR-PLETDRPLTLQERLIRKLGANAYPFYFVPPHCPA 124
QY 126 SVTLQOGEEDNDGDPCCGVSYVYKIFAGESETDTRHSTVTTLGIRKIQFAPTKQGOQCTL 185
DB 125 SVSLQAPAPGDTGKPCGVDTYELKAFVGESEDEKPHKNSVRLAIRKIMYAPSKLGEQPSIE 184
QY 186 VRKDFMLSPGELLEVTLQKLYLHGERIGVNICIRNSNMVKKIKAMVQGVVLFQ 245
DB 185 VSKEYILKPKNHLEASLDKELHYHGESLSVNVHIANSSKTVKIKVSVRFADICLFS 244
QY 246 NSGYRNTVASLETSECPPIQGSSTQKVMYLPPLSSNKQRGIALDGOIKRQDCLAST 305
DB 245 TAQYKCTVAEVESEDCQVAPGFTLSKVFLLPLANKXDKWGLALDGLKHEDTNLASS 304
QY 306 TLLAOPDQDAFGVYIISYAVKYLFLGALGELSAELPFVLMHPKPGTRAKVI 358
DB 305 TLLADPSQRENLCIIVQYKVKLCITPLGDLVAELPFILMHPKPDDEPVI 357

RESULT 9
Q66GU6 PRELIMINARY; PRT; 398 AA.

ID Q66GU6
AC Q66GU6; PRELIMINARY; PRT; 398 AA.
DT 25-OCT-2004 (Tremblrel. 28, Created)
DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)
DE Arrestin 2-like protein Artr2.
GN Name=ARR2;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_Taxid=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RX MEDLINE=23159591; PubMed=14986925;
RA Merrill C.E.; Pitts R.J.; Zwebel L.J.;
RT "Molecular characterization of arrestin family members in the malaria
vector mosquito, Anopheles gambiae.";
RL Insect Mol. Biol. 12:641-650(2003).
DR EMBL; BK000996; DA000888.1;
DR InterPro; IPR000698; Arrestin.
DR InterPro; IPR011022; Arrestin.
DR Pfam; PF02752; Arrestin_C; 1.
DR PRINTS; PR00309; Arrestin_N; 1.
DR PRODOM; PD002099; Arrestin; 2.
DR PROSITE; PS00295; Arrestin; 1.
SQ SEQUENCE 398 AA; 44536 MW; 73DD73FB34F01418 CRC64;

Query Match
Best Local Similarity 51.8%; Score 1023; DB 2; Length 398;
Matches 191; Conservative 75; Mismatches 85; Indels 2; Gaps 2;

Matches 204; Conservative 65; Mismatches 111; Indels 10; Gaps 7;

QY 1 MVYNFVKKCAPNGKVTLYMGKRDVDSGVPEPIDGIVLDDERYTRDNKRVGQIVCS 60
DB 1 MVAVKVFVKCAPNGKLTLYLGKRDVDFHITHVDPIDGVVLDIDPDYKE-RKVFGLHAFRYGR 65
QY 61 FRYGREDEVMGLNFOKELCLASEQIYPRPEKSDKEQTKLOERLKLGSNAIPFTFNIS 120
DB 60 YRYGREDEVMGLNFOKELCLASEQIYPRPEKSDKEQTKLOERLKLGSNAIPFTFNIS 120
QY 121 PNAPSVTLQOGEEDNDGDPCCGVSYVYKIFAGESETDTRHSTVTTLGIRKIQFAPTKQGO 180
DB 119 SNAPSVTLQOGEEDNDGDPCCGVSYVYKIFAGESETDTRHSTVTTLGIRKIQFAPTKQGO 180
QY 181 Q-PCTLVKRDVLSPELEVTLDKQLYLHGERIGVNICIRNSNMVKKIKAMVQGVVLFQ 245
DB 179 RLPSSLSVSKFTFSQKINLEVTLDREITYHGEKIANIVVTTNSRKTVKSIKCFVQHC 238
QY 240 DVTLFONGSVYRNTVASLETSECPPIQGSSTQKVMYLPPLSSNKQRGIALDGOIKRQD 299
DB 239 EVTMV-NAQFSKHIALSLETREGCPTTPGASFTKSFLLVPLASSNKQRGIALDGHLEDD 297
QY 300 QCLASTTLLAOPD-QRDAFGVYIISYAVKYLFLGALGELSAELPFVLMHPKPGT--KAK 356
DB 298 VNLASTTLLISECKPSPDMGIVISLRKVLNCGTLGGLQTDVPEKLMNPAGSVVERER 357
QY 357 VIHADSQADVETFRQDT--IDQASVDFE 383
DB 358 VNALKKMSIERHRYENSHYADDDDNIVEE 387

RESULT 10

ID Q705Q8 PRELIMINARY; PRT; 401 AA.

ID Q705Q8
AC Q705Q8; PRELIMINARY; PRT; 401 AA.
DT 01-MAR-2004 (Tremblrel. 26, Created)
DT 01-MAR-2004 (Tremblrel. 26, Last sequence update)
DE AgCP5798 (Fragment).
GN Name=agCG52387; ORFNames=ENSANG00000018139;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_Taxid=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008960; EAA10755.1;
DR HSSP; P17870; 1G4M.
DR GO; GO:0007600; P:sensory perception; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000698; Arrestin.
DR InterPro; IPR011022; Arrestin.
DR Pfam; PF02752; Arrestin_C; 1.
DR PRINTS; PR00309; Arrestin_N; 1.
DR PRODOM; PD002099; Arrestin; 2.
DR PROSITE; PS00295; Arrestin; 1.
FT NON_TER 1
SQ SEQUENCE 401 AA; 44862 MW; F307885989AC4EE4 CRC64;

Query Match
Best Local Similarity 52.3%; Score 1023; DB 2; Length 401;
Matches 204; Conservative 65; Mismatches 111; Indels 10; Gaps 7;

QY 1 MVYNFVKKCAPNGKVTLYMGKRDVDSGVPEPIDGIVLDDERYTRDNKRVGQIVCS 60
DB 1 MVAVKVFVKCAPNGKLTLYLGKRDVDFHITHVDPIDGVVLDIDPDYKE-RKVFGLHAFRYGR 65
QY 61 FRYGREDEVMGLNFOKELCLASEQIYPRPEKSDKEQTKLOERLKLGSNAIPFTFNIS 120
DB 60 YRYGREDEVMGLNFOKELCLASEQIYPRPEKSDKEQTKLOERLKLGSNAIPFTFNIS 120
QY 121 PNAPSVTLQOGEEDNDGDPCCGVSYVYKIFAGESETDTRHSTVTTLGIRKIQFAPTKQGO 180
DB 119 SNAPSVTLQOGEEDNDGDPCCGVSYVYKIFAGESETDTRHSTVTTLGIRKIQFAPTKQGO 180
QY 181 Q-PCTLVKRDVLSPELEVTLDKQLYLHGERIGVNICIRNSNMVKKIKAMVQGVVLFQ 245
DB 179 RLPSSLSVSKFTFSQKINLEVTLDREITYHGEKIANIVVTTNSRKTVKSIKCFVQHC 238
QY 240 DVTLFONGSVYRNTVASLETSECPPIQGSSTQKVMYLPPLSSNKQRGIALDGOIKRQD 299
DB 239 EVTMV-NAQFSKHIALSLETREGCPTTPGASFTKSFLLVPLASSNKQRGIALDGHLEDD 297
QY 300 QCLASTTLLAOPD-QRDAFGVYIISYAVKYLFLGALGELSAELPFVLMHPKPGT--KAK 356
DB 298 VNLASTTLLISECKPSPDMGIVISLRKVLNCGTLGGLQTDVPEKLMNPAGSVVERER 357
QY 357 VIHADSQADVETFRQDT--IDQASVDFE 383
DB 358 VNALKKMSIERHRYENSHYADDDDNIVEE 387

DR FlyBase; FBgn0040206; krz.
 DR GO; GO:0007600; P:sensory perception; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR000698; Arrestin.
 DR InterPro; IPR011022; Arrestin_C.
 DR InterPro; IPR011021; Arrestin_N.
 DR Pfam; PF02752; Arrestin_N.
 DR Pfam; PF00339; Arrestin_C; 1.
 DR PRINTS; PR00309; Arrestin_N; 1.
 DR PROSITE; PS00295; ARRESTIN.
 DR PROSITE; PS00295; ARRESTINS; 1.
 SQ SEQUENCE 470 AA, 51237 MW, FEP954324007C26A CRC64;

Query Match
 Best Local Similarity 50.8%; Score 1002; DB 2; Length 470;
 Matches 187; Conservative 70; Mismatches 87; Indels 4; Gaps 3;

QY 6 KVEKCCAPNGKVTLYMGKRDVHVSQVEPIIDGIVLDDIYIRDNKRVFGQIVCSFRYGR 65
 DB 48 RVEFKSSSSNGKITVYLGKRDVHVSQVEPIIDGIVLDDIYIRDNKRVFGQIVCSFRYGR 65
 QY 66 EEDEVMGINFOKELCCLASEQIYPRPEKSDKEQTKLOERLLKLGSAIPTFNISPNAPS 106
 DB 107 EDLDVLGLTRKDLVLAHEQIYPRPEKSDKEQTKLOERLLKLGSAIPTFNISPNAPS 125
 QY 126 SVTLQOGEEDNDGPGVSVYVKIFAGESEETDRTRRSVTTLGIRKIQEAPTKOGQOQCTL 165
 DB 166 SVSLQAPGPDVSKGCVDEYELKAFGEENVEDKPKRNSVRLTTRKVMYAPSKVGEQPSIE 185
 QY 186 VRKDFMLSPGELELEVTLDKOLYLHGERIGVNICIRNNSNMVKIKAMVQGVVDVVLFG 225
 DB 226 VSKFEMKPKNIHLKATLDELKELHYHGEKISVNVHANNNSNRTYKIKVCVRQFADICLS 245
 QY 246 NSGYRNTVASLETSEGCPIQPGSSLOKVMYLTPLSSNKQRGIALDQIKRODOCLAST 285
 DB 286 TAQKSVVAEISEDEGQVAPGFULSKVFEELCPULANNKDKMGLALDQIKHEDNVLAS 305
 QY 306 TLLAQPDQDAFGVLIISYAVKVLFLGA--LGSELSAELPFLMHKPK 351
 DB 346 TLITNPAQRESLGIWVHYKVKVLLISSPLNGDLVALLEPFTLMHHPK 393

RESULT 12
 ARRB LOCMI

ID ARRB LOCMI STANDARD; PRT; 407 AA.
 AC P32132;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DE 15-JUL-1999 (Rel. 38, Last annotation update)
 OS Arrestin homolog.
 OS Locusta migratoria (Migratory locust).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.
 OX NCBI_TaxID=7004;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Antenna;
 RX MEDLINE=93199955; PubMed=8452755; DOI=10.1016/0898-6568(93)90009-B;
 RA Raming K., Freitag J., Krieger J., Breer H.;
 RT "Arrestin-subtypes in insect antennae";
 RL Cell. Signal. 5:69-80(1993).
 CC -1- SIMILARITY: Belongs to the arrestin family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/)
 CC or send an email to license@isb-sib.ch).
 CC EMBL; S57174; AAB25860.1; -
 DR PIR; A56607; A56607.

DR HSSP; P17870; 1G4M.
 DR InterPro; IPR000698; Arrestin.
 DR InterPro; IPR011022; Arrestin_C.
 DR InterPro; IPR011021; Arrestin_N.
 DR Pfam; PF02752; Arrestin_N.
 DR Pfam; PF00339; Arrestin_C; 1.
 DR PRINTS; PR00309; Arrestin_N; 1.
 DR PRODOM; PD002099; Arrestin; 2.
 DR PROSITE; PS00295; ARRESTINS; 1.
 KW Sensory transduction.
 SQ SEQUENCE 407 AA, 45543 MW, DEC28A3A534935BB CRC64;

Query Match
 Best Local Similarity 50.4%; Score 993.5; DB 1; Length 407;
 Matches 202; Conservative 64; Mismatches 107; Indels 15; Gaps 8;

QY 6 KVEKCCAPNGKVTLYMGKRDVHVSQVEPIIDGIVLDDIYIRDNKRVFGQIVCSFRYGR 65
 DB 14 KVEKCTTPNGKVTLYMGKRDVHVSQVEPIIDGIVLDDIYIRDNKRVFGQIVCSFRYGR 72
 QY 66 EEDEVMGINFOKELCCLASEQIYPRPEKSDKEQTKLOERLLKLGSAIPTFNISPNAPS 125
 DB 73 EEDEVMGINFOKELCCLASEQIYPRPEKSDKEQTKLOERLLKLGSAIPTFNISPNAPS 131
 QY 126 SVTLQOGEEDNDGPGVSVYVKIFAGESEETDRTRRSVTTLGIRKIQEAPTKOGQOQCTL 184
 DB 132 SVTLQPGDDDGKPLGVEYSVKTWGDHAEKHKRSVTLAIKQLQVAPTRGRRLPSS 191
 QY 185 LVRKDFMLSPGELELEVTLDKOLYLHGERIGVNICIRNNSNMVKIKAMVQGVVDVVLFG 244
 DB 192 LVSKGFTESSQKINLEVTLDREIYHGEKLANVLIINNRSKTVKIKVYVVOHCEVTMV 251
 QY 245 QNGSYRNTVASLETSEGCPIQPGSSLOKVMYLTPLSSNKQRGIALDQIKRODOCLAS 304
 DB 252 -NAQFSRHVASLETREGCPIPGASFTVYFVLPCAASNKDRYGIALDQIKRODOCLAS 310
 QY 305 TLLAQ-PDQDAFGVLIISYAVKVLFLGALGSELPAELPFLMHKPKGT---KAKVTH 359
 DB 311 STLVSQKNTDAIGIVISYSLRVKLCNGTLGSELQTDVPPFKLHPAPGTAEREKAQAI- 369
 QY 360 ADSQADVETFRQD---TIDQASVDPE 383
 DB 370 -KKMSIERTRYENSCYAADDNDNIVFE 396

RESULT 13
 ARRB DROME

ID ARRB DROME STANDARD; PRT; 401 AA.
 AC P19107; Q9VSN6;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DE 25-JAN-2005 (Rel. 46, Last annotation update)
 GN Phosrestin I (Arrestin B) (Arrestin 2) (49 kDa arrestin-like protein).
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=90232360; PubMed=2158671;
 RA Yamada T., Takeuchi Y., Kuroi N., Kobayashi H., Sakai Y., Hotta Y.,
 RA Matsunoto H.;
 RT "A 49-kilodalton phosphoprotein in the Drosophila photoreceptor is an
 RT arrestin homolog";
 RL Science 248:483-486(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Bailew R.M., Baas A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Chery J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieria S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mlehnina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svitek R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
[3]
RP GENOME REANNOTATION.
RX MEDLINE=22426069; PubMed=12537572;
RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettecourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
[4]
RP PHOSPHORYLATION, AND PROBABLE FUNCTION.
RX MEDLINE=91282780; PubMed=1905538;
RA Matsumoto H., Yamada T.;
RT "Phosrestins I and II: arrestin homologs which undergo differential
RT light-induced phosphorylation in the Drosophila photoreceptor in
RT vivo.";
RL Biochem. Biophys. Res. Commun. 177:1306-1312(1991).
[5]
RP PHOSPHORYLATION SITE SER-366.
RX MEDLINE=94242441; PubMed=8185954; DOI=10.1016/0896-6273(94)90309-3;
RA Matsumoto H., Kurten B.T., Takagi Y., Kahn E.S., Kinumi T., Komori N.,
RA Yamada T., Hayashi F., Isono K., Pak W.L.;
RT "Phosrestin I undergoes the earliest light-induced phosphorylation by
RT a calcium/calmodulin-dependent protein kinase in Drosophila
RT photoreceptors.";
RL Neuron 12:997-1010(1994).
CC -1- FUNCTION: Probably plays an important role in the photoreceptor
CC transduction.
CC -1- TISSUE SPECIFICITY: Inner and outer segments, and the inner
CC plexiform regions of the retina.
CC -1- PTM: Phosphorylated upon light exposure.
CC -1- SIMILARITY: Belongs to the arrestin family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL; M32141; AAA28833.1; -.
DR EMBL; AE003554; AAF50380.1; -.
DR PIR; A34856; A34856.
DR HSSP; P17870; 1G4M.
DR FlyBase; FBgn000121; Arr2.
DR GO; GO:0005624; C:membrane fraction; IDA.
DR GO; GO:0016028; C:ribosome; IDA.
DR GO; GO:0005625; C:soluble fraction; IDA.
DR GO; GO:0016060; P:metarhodopsin inactivation; IMP.
DR InterPro; IPR000698; Arrestin.
DR InterPro; IPR011022; Arrestin_C.
DR InterPro; IPR011021; Arrestin_N.
DR Pfam; PF02752; Arrestin_C; 1.
DR Pfam; PF00339; Arrestin_N; 1.
DR PRINTS; PR00309; ARRESTIN.
DR ProDom; PD002099; Arrestin; 2.
DR PROSITE; PS00295; ARRESTIN; 1.
KW Phosphorylation; Sensory transduction; Vision.
FT MOD_RES 366 366 Phosphoserine (by CAMK).
FT VARIRT 109 109 N -> S.
FT CONFLICT 111 111 Y -> H (in Ref. 1).
SQ SEQUENCE 401 AA; 45028 MW; 12C776E0DA8F0D87 CRC64;

Query Match 49.8%; Score 982.5; DB 1; Length 401;
Best Local Similarity 48.7%; Pred. No. 8.3e-68;
Matches 191; Conservative 73; Mismatches 115; Indels 13; Gaps 6;

QY 1 MVTNFKVKKCAPNGKVTLYMGKDPVDHVSQVEPIDGIVLDDXYIRNRKVFQIVCS 60
DB 1 MVTNFKVKKCAPNGKVTLYMGKDPVDHVSQVEPIDGIVLDDXYIRNRKVFQIVCS 59
61 FRYGREDEVMGLNFOKEICLASEQIYPRPEKSDKEQTKLQERLLKLGSAIPTFNIS 120
DB 60 YRYGREDEVMGVKFSKEILLCREQIVP-TNPMEWETPMQEKLVKLGSAIYPTFHFP 118
121 PNAPSSVTLQGGEDDNGPCGVSYVVKIFAGESETDRHRSVTTLGIRKIQFAPTKGQ 180
DB 119 PNAPSSVTLQGGEDDNGPCGVSYVVKIFAGESETDRHRSVTTLGIRKIQFAPTKGQ 178
181 Q-PCTIVRKDFMLSPGELEVTLDKQLYLGERIGVNICIRNSNKNVKKIKAMVQGV 239
DB 179 RLPSSLSVKGFTFSPNGKISLEVTLDREIYHGEKTAATVQVSNNSKSVSICKFIVQHT 238
240 DVLFPQNGSYRNTVASLETSEGCPIQPGSSLOKVMYLTPLSSNKQRRGIALDGOIKRD 299
DB 239 EITMV-NAQFSKHAQAQLETKEGCPTTPGANLTKTFYLLPLAANNKDRHGIALDGLKDED 297
QY 300 QCLASTTLLAQ-PDQDAFGVIISYAVKVLFLGALGGEISAE LPPVLMHPKPGT----- 353
DB 298 VNLASSTWQEGKSTGDACGIVISYSVRKILNCGTLGEMQTDVFPKLLQAPAGTIEKKR 357
QY 354 ---KAKVIHADSDADVETFRQDTIDQASVDF 382
DB 358 SNAMKKMKSIEQHRNVKGYQDDDDNDIVFEDF 389

RESULT 14
ARRB_DROMI
ID ARRB_DROMI STANDARD; PRT; 401 AA.
AC P19108;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Phosrestin I (Arrestin B) (Arrestin 2) (49 kDa arrestin-like protein).
GN Name=Arr2; Synonyms=ArrB;

OS Drosophila miranda (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7229;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S204;
RX MEDLINE=91016944; PubMed=2216789;
RA Krishnan R., Ganguly R.;
RT "Nucleotide sequence of the arrestin-like 49 Kd protein gene of
RL Drosophila miranda."
RU Nucleic Acids Res. 18:5894-5894(1990).
CC -1- FUNCTION: Undergoes light-induced phosphorylation, probably plays
CC an important role in the photoreceptor transduction.
CC -1- TISSUE SPECIFICITY: Inner and outer segments, and the inner
CC plexiform regions of the retina.
CC -1- SIMILARITY: Belongs to the arrestin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X54084; CAA38019.1; --
DR PIR; S11566; S11566.
DR HSSP; P17870; 1G4M.
DR FlyBase; FBgn0012552; Dmir\Arr2.
DR InterPro; IPR000698; Arrestin.
DR InterPro; IPR011022; Arrestin_C.
DR InterPro; IPR011021; Arrestin_N.
DR Pfam; PF02752; Arrestin_C; 1.
DR Pfam; PF00339; Arrestin_N; 1.
DR PRINTS; PR00309; ARRESTIN.
DR ProDom; PD002099; Arrestin; 2.
DR PROSITE; PS00295; ARRESTINS; 1.
DR Phosphorylation; Sensory transduction; Vision.
KW SEQUENCE 401 AA; 45014 MW; E46EBC2485AF99C CRC64;
SQ
Query Match
Best Local Similarity 49.5%; Score 977.5; DB 1; Length 401;
Matches 190; Conservative 76; Mismatches 113; Indels 13; Gaps 6;
QY 1 MVTNFKVFKKCAPNGKVTLYMGKDPVDHVGVEPIDGIYVLDEYIRDNKRVGQIVCS 60
DB 1 MVTNFKVFKKCAPNGKVTLYMGKDPVDHVGVEPIDGIYVLDEYIRDNKRVGQIVCS 60
QY 61 FRYGREDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKLGSNAPFTFNIS 120
DB 60 FRYGREDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKLGSNAPFTFNIS 120
QY 121 PNAPSSVTLQOGEEDNGDPCGVSYVYKIFAGESETDRTHRSVTYTLGIRKIQFAPTKQO 180
DB 119 PNAPSSVTLQOGEEDNGDPCGVSYVYKIFAGESETDRTHRSVTYTLGIRKIQFAPTKQO 180
QY 181 Q-PCTLVKDFMLSPGELLEVTLDKQLYLHGERIGVNICIRNNSNMVKKIKAMVQOGV 239
DB 179 RLPSSLVSKGFTFNGKISLEVTLDREIYYHGEKTAATVQVSNNSKSVKSIKCIIVQHT 238
QY 240 DVLFQNGSYRNTVASLETSEGCPIQPGSSLOKVMYLTPLLSNKKORGIALDGOIKROD 299
DB 239 EITMV-NAQFSKHAQALETKEGCPITPGANLTKTFYLIPLAANNDRHGIALDGLKDED 297
QY 300 QCLASTTLAQQ-PDQDAFGVYISYAVKYLFLGALGELSAELPFLMHKPKGT----- 353
DB 298 VNLAASSTWQEGKNTGDACGIVISYVRIKLCNGCITLGGEMQTVPFKLPAPGTIEKKR 357
QY 354 ---KAKVIHADSQADVETFRQDTIDQASVDF 382
DB 358 SNAMKMKSIQHRNVKGYQDDDDNIVFEDF 389

RESULT 15
ARB_CALVI
ID ARRB CALVI STANDARD; PRT; 400 AA.
AC P51487;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Phorestin I (Arrestin B) (Arrestin 2).
GN Name=ARR2;
OS Calliphora vicina (Blue blowfly) (Calliphora erythrocephala).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=7373;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-10.
RC TISSUE=Retina;
RX MEDLINE=95014564; PubMed=7929436;
RA Planger A., Malicki D., Whitney M., Paulsen R.;
RT "Mechanism of arrestin 2 function in rhabdomic photoreceptors."
RL J. Biol. Chem. 269:26969-26975(1994).
CC -1- FUNCTION: Directly interacts with light-activated rhodopsin
CC thereby activating the phosphorylation of metarhodopsin. Inhibits
CC the dephosphorylation of metarhodopsin.
CC -1- SIMILARITY: Belongs to the arrestin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X79073; CAA55673.1; --
DR PIR; B55081; B55081.
DR HSSP; P17870; 1G4M.
DR InterPro; IPR000698; Arrestin.
DR InterPro; IPR011022; Arrestin_C.
DR InterPro; IPR011021; Arrestin_N.
DR Pfam; PF02752; Arrestin_C; 1.
DR Pfam; PF00339; Arrestin_N; 1.
DR PRINTS; PR00309; ARRESTIN.
DR ProDom; PD002099; Arrestin; 2.
DR PROSITE; PS00295; ARRESTINS; 1.
DR Direct protein sequencing; Phosphorylation; Sensory transduction;
KW Vision.
FT INIT MET
SQ SEQUENCE 400 AA; 44781 MW; DA786D7E9FFB4A29 CRC64;
Query Match
Best Local Similarity 47.6%; Score 937.5; DB 1; Length 400;
Matches 186; Conservative 70; Mismatches 122; Indels 13; Gaps 6;
QY 2 VYNFKVFKKCAPNGKVTLYMGKDPVDHVGVEPIDGIYVLDEYIRDNKRVGQIVCSF 61
DB 1 VVSVKVFKAATPNGKVTLYLGRHRIDHFDYIDVDGVIVDPDYLK-NRKVFAQLATY 59
QY 62 RYGREDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKLGSNAPFTFNIS 121
DB 60 RYGREDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKLGSNAPFTFNIS 118
QY 122 NAPSSVTLQOGEEDNGDPCGVSYVYKIFAGESETDRTHRSVTYTLGIRKIQFAPTKQO 181
DB 119 NSPSSVTLQOGEEDLGLKPLGVEYITRAYVADSEDDRQHKRSWVSLVTKLQYAPPTRGQR 178
QY 182 -PCTLVKDFMLSPGELLEVTLDKQLYLHGERIGVNICIRNNSNMVKKIKAMVQOGVD 240
DB 179 LPSLSLVSKGFTFNGKISLEVTLDREIYYHGEKTAATVQVSNNSKAVNKKVFIQHT 238
QY 241 VVLFQNGSYRNTVASLETSEGCPIQPGSSLOKVMYLTPLLSNKKORGIALDGOIKROD 300

Db	239	ITMV-NAQFSKHVAQLETKEGCPIITPGANLSKTFYLLIPLASNNKDRHIGIALDGHLCDEBV	297
Qy	301	CLASTLLAQ-PDQRDAFGVITISYAVKVKLFLGALGELSLELPFVLMHPKPGT-----	353
Db	298	NLASSTWQDGKSTGDAGIVISYSVRILKNCGLGGEIQTDPFVKLLQPAFGSVEKKRS	357
Qy	354	--KAKYIHADSQADVETFRQDTIDQQASVDF	382
Db	358	NAMKKMSIEQHRNTKGYQDDDDNIVFEDF	388

Search completed: February 9, 2005, 23:45:33
Job time : 66 secs

This Page Blank (uspto)

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 9, 2005, 23:18:51 ; Search time 165 Seconds
(without alignments)
897.753 Million cell updates/sec

Title: US-10-056-405-2

Perfect score: 1973
Sequence: 1 MVYMFKVKFKKCAPNGKVTLY.....ADVETFRQDTIDQASVDFE 383

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp19808:*
2: geneseqp19908:*
3: geneseqp20008:*
4: geneseqp20018:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp20038:*
8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1973	100.0	383	5	ABP52833	Abp52833 Anopheles
2	1973	100.0	383	7	ABR84476	AbR84476 Mosquito
3	1384	70.1	364	4	ABB61736	Abb61736 Drosophila
4	1384	70.1	364	8	ADQ89588	Adq89588 Antagonis
5	1023	51.8	398	7	ABR84484	ABr84484 Mosquito
6	1002	50.8	470	4	ABB58174	Abb58174 Drosophila
7	982.5	49.8	401	4	ABB61964	Abb61964 Drosophila
8	907.5	46.0	410	4	AA667780	AAg67780 Amino aci
9	903.5	45.8	418	4	AA667778	AAg67778 Amino aci
10	903.5	45.8	452	5	ABG69495	ABg69495 Rat bait
11	900.5	45.6	418	5	ABG70174	ABg70174 Human pre
12	900.5	45.6	418	8	ADQ89786	Adq89786 Antagonis
13	897.5	45.5	418	4	AA667779	AAg67779 Amino aci
14	890	45.1	369	4	ABG13574	ABg13574 Novel hum
15	885	44.9	382	4	AA667785	AAg67785 An. exempl
16	885	44.9	409	4	AA667781	AAg67781 Amino aci
17	885	44.9	409	7	AD58183	Ad58183 Human Pro
18	885	44.9	409	7	AD58179	Ad58179 Human Pro
19	885	44.9	409	7	ADN95251	Adn95251 Human BEC
20	880	44.6	409	6	AA667784	AAg67784 An. exempl
21	874	44.3	360	6	ADA00635	Ada00635 Human bet
22	874	44.3	495	6	ADA00637	Ada00637 Human bet
23	869.5	44.1	410	5	ABG69496	ABg69496 Rat bait
24	869.5	44.1	410	7	AD58177	Ad58177 Rat Prote
25	869.5	44.1	410	7	AD58181	Ad58181 Rat Prote

26	869.5	44.1	526	8	ADR23187	Adr23187 Yellow fl
27	869.5	44.1	526	8	ADR23188	Adr23188 Green fl
28	869.5	44.1	526	8	ADR23186	Adr23186 Yellow fl
29	865	43.8	454	8	ADN24049	Adn24049 Bacterial
30	780.5	39.6	388	4	AA667783	AAg67783 Amino aci
31	780	39.5	405	4	AA667783	AAg67783 Amino aci
32	779.5	39.5	388	4	AA667782	AAg67782 Amino aci
33	761	38.6	405	8	ADQ14327	Adq14327 Human ret
34	761	38.6	405	8	ADR41708	Adr41708 Protein s
35	661	33.5	468	4	AA667747	AAm79747 Human pro
36	516.5	26.2	182	7	ADD27419	Add27419 Human adl
37	516.5	26.2	182	7	ADD27127	Add27127 Human adl
38	516.5	26.2	187	6	ABU70623	Abu70623 Human adl
39	516.5	26.2	187	7	ADD27507	Add27507 Human adl
40	497.5	25.2	180	6	ADA00634	Ada00634 Human bet
41	497.5	25.2	315	6	ADA00636	Ada00636 Human bet
42	482.5	24.5	182	7	ADD27197	Add27197 Human adl
43	361.5	18.3	212	4	AA673899	AAg73899 Human col
44	351.5	17.8	456	4	ABB58949	Abb58949 Drosophila
45	173	8.8	65	4	ABB42223	Abb42223 Peptide #

ALIGNMENTS

RESULT 1	ABP52833	ABP52833 standard; protein; 383 AA.
ID	ABP52833	
XX	AC	ABP52833;
XX	AC	
DT	01-NOV-2002	(first entry)
XX	XX	
DE	Anopheles gambiae	arrestin 1 protein SEQ ID NO:2.
XX	XX	
KW	Anopheles gambiae;	mosquito; olfactory gene; arrestin 1; pest control;
KW	odourant receptor;	olfaction.
XX	XX	
OS	Anopheles gambiae.	
XX	XX	
PN	W0200259274-A2.	
XX	XX	
PD	01-AUG-2002.	
XX	XX	
PF	28-JAN-2002;	2002WO-US002549.
XX	XX	
PR	26-JAN-2001;	2001US-0264649P.
XX	XX	
PR	24-JAN-2002;	2002US-00056405.
XX	XX	
PA	(UYVA-) UNIV VANDERBILT.	
XX	XX	
PI	Zwiebel LJ;	
XX	XX	
DR	WPI; 2002-627421/67.	
DR	N-PSDB; ABQ75102.	
XX	XX	
PT	New mosquito olfaction polypeptides and polynucleotides, useful for	
PT	mosquito management, i.e. controlling the pest and disease vectors, or	
PT	for identifying pest control agents.	
XX	XX	
PS	Claim 18; Fig 2; 96pp; English.	
XX	XX	
CC	The present invention describes a purified Anopheles gambiae olfaction	
CC	polypeptide comprising a 383, 394, 380, 411, 412, 391, 157 or 401 residue	
CC	amino acid sequence (see ABP52833 to ABP52840) (S1), a conservatively	
CC	modified amino acid sequence of them, or a sequence of (S1) with at least	
CC	20 consecutive residues. Also described: (1) an isolated polynucleotide	
CC	comprising: (a) a nucleotide sequence encoding the purified Anopheles	
CC	gambiae olfaction polypeptide; or (b) a nucleotide sequence that	
CC	hybridises under stringent conditions to a hybridisation probe comprising	
CC	a 1964, 1239, 1142, 1236, 1194, 1176, 474 or 1206 nucleotide sequence	
CC	(see ABQ75102 to ABQ75105 and ABQ75110 to ABQ75113) (S2), or its	
CC	complement; and (2) a method for identifying an agent that binds to	

CC mosquito olfaction molecules comprising: (a) providing an isolated;
CC mosquito olfaction molecule; (b) contacting a test agent with the
CC isolated mosquito olfaction molecule; and (c) detecting specific binding
CC of the test agent to the isolated mosquito olfaction molecule, where the
CC presence of specific binding identifies the test agent as a mosquito
CC olfaction-binding compound. The mosquito olfaction molecule, where the
CC method from the present invention of screening this pest and disease vector
CC modulate arrestin-odourant receptor interaction for substances that
CC pest control agents. The present sequence represents Anopheles gambiae
CC arrestin 1 from the present invention
XX
SQ Sequence 383 AA;

Query Match
Best Local Similarity 100.0%; Score 1973; DB 5; Length 383;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYNFKVFKKCAPNGKVTLYMGRDFVDHVSVEPIDGIVLDEYIRDNKRVFGQIVCS 60
DB 1 MYNFKVFKKCAPNGKVTLYMGRDFVDHVSVEPIDGIVLDEYIRDNKRVFGQIVCS 60
QY 61 FRYGREDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKLGSNAPFTENIS 120
DB 61 FRYGREDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKLGSNAPFTENIS 120
QY 121 PNAPSSVTLLQOGEDNDGDCGVSYVYKIFAGESETDRTHRSTVTLGIRKIQFAPTKQOQ 180
DB 121 PNAPSSVTLLQOGEDNDGDCGVSYVYKIFAGESETDRTHRSTVTLGIRKIQFAPTKQOQ 180
QY 181 QPCTLVKDFMLSPGELLEVTLDKQLYLHGERIGVNICIRNNSNMVKKIKAMVQOQVD 240
DB 181 QPCTLVKDFMLSPGELLEVTLDKQLYLHGERIGVNICIRNNSNMVKKIKAMVQOQVD 240
QY 241 VVLFONGSYRNTVASLETSEGCPIOPGSSLOKVMYLTPLSSNKORRGIALDGOIKRODQ 300
DB 241 VVLFONGSYRNTVASLETSEGCPIOPGSSLOKVMYLTPLSSNKORRGIALDGOIKRODQ 300
QY 301 CLASTTLLAOPDORDAFGVIIISYAVKVLFLGALGELSALPFLVLMHPKPGTKAKAVIHA 360
DB 301 CLASTTLLAOPDORDAFGVIIISYAVKVLFLGALGELSALPFLVLMHPKPGTKAKAVIHA 360
QY 361 DSQADVETFRQDTIDQASVDPE 383
DB 361 DSQADVETFRQDTIDQASVDPE 383

RESULT 2
ID ABR84476 standard; protein; 383 AA.
XX ABR84476;
AC ABR84476;
DT 15-JAN-2004 (first entry)
XX
DE Mosquito olfaction molecule, arrestin 1.
XX
KW Arrestin 1; mosquito; olfaction; insecticide; antimalarial.
XX
OS Anopheles gambiae.
XX
PN WO2003076590-A2.
XX
PD 18-SEP-2003.
XX
PF 10-MAR-2003; 2003WO-US007174.
XX
PR 08-MAR-2002; 2002US-00094240.
XX
PA (UYVA-) UNIV VANDERBILT.
XX
PI Zwiebel LJ;
XX

DR WPI; 2003-722331/68.
DR N-PSDB; ACF79716.
XX
PT New mosquito arrestin 1 and 2 genes and polypeptides, useful for
PT identifying mosquito olfaction molecule binding compounds which reduce
XX the ability of mosquitoes to locate sources of bloodmeal, e.g. humans.
PS Claim 1; Fig 2; 101pp; English.
XX
CC The present sequence is the protein sequence of arrestin 1, a novel
CC mosquito olfaction molecule. The invention provides 9 novel mosquito
CC polypeptides and the nucleic acids encoding them. These are arrestins 1
CC and 2 and odorant receptor molecules 1-7. The odorant receptors 1
CC in a ligand-induced signal transduction pathway for the activation of
CC mosquito olfaction. Arrestin functions to inhibit the activated signal
CC and arrestin as an 'off' switch for the odorant receptors act as an 'on' switch,
CC with the operation of the mosquito olfactory system, particularly
CC compounds that modulate arrestin 2 activity. These are useful for the
CC control of mosquitoes, particularly by reducing their ability to locate
CC sources of bloodmeal
SQ Sequence 383 AA;

Query Match
Best Local Similarity 100.0%; Score 1973; DB 7; Length 383;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYNFKVFKKCAPNGKVTLYMGRDFVDHVSVEPIDGIVLDEYIRDNKRVFGQIVCS 60
DB 1 MYNFKVFKKCAPNGKVTLYMGRDFVDHVSVEPIDGIVLDEYIRDNKRVFGQIVCS 60
QY 61 FRYGREDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKLGSNAPFTENIS 120
DB 61 FRYGREDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKLGSNAPFTENIS 120
QY 121 PNAPSSVTLLQOGEDNDGDCGVSYVYKIFAGESETDRTHRSTVTLGIRKIQFAPTKQOQ 180
DB 121 PNAPSSVTLLQOGEDNDGDCGVSYVYKIFAGESETDRTHRSTVTLGIRKIQFAPTKQOQ 180
QY 181 QPCTLVKDFMLSPGELLEVTLDKQLYLHGERIGVNICIRNNSNMVKKIKAMVQOQVD 240
DB 181 QPCTLVKDFMLSPGELLEVTLDKQLYLHGERIGVNICIRNNSNMVKKIKAMVQOQVD 240
QY 241 VVLFONGSYRNTVASLETSEGCPIOPGSSLOKVMYLTPLSSNKORRGIALDGOIKRODQ 300
DB 241 VVLFONGSYRNTVASLETSEGCPIOPGSSLOKVMYLTPLSSNKORRGIALDGOIKRODQ 300
QY 301 CLASTTLLAOPDORDAFGVIIISYAVKVLFLGALGELSALPFLVLMHPKPGTKAKAVIHA 360
DB 301 CLASTTLLAOPDORDAFGVIIISYAVKVLFLGALGELSALPFLVLMHPKPGTKAKAVIHA 360
QY 361 DSQADVETFRQDTIDQASVDPE 383
DB 361 DSQADVETFRQDTIDQASVDPE 383

RESULT 3
ID ABB61736 standard; protein; 364 AA.
XX ABB61736;
AC ABB61736;
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 12000.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
XX
OS Drosophila melanogaster.
XX

PN WO200171042-A2.
XX
XX 27-SEP-2001.
PD
XX
XX 23-MAR-2001; 2001WO-US009231.
PF
XX
XX 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
XX (PEKE) PE CORP NY.
PA
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
PI
XX WPI; 2001-656860/75.
DR N-PSDB; ABL05839.
XX
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
XX
PS Disclosure; SEQ ID NO 12000; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (AB57737-
CC AB872072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 364 AA;

Query Match 70.1%; Score 1384; DB 4; Length 364;
Best Local Similarity 70.3%; Pred. No. 1.5e-135;
Matches 258; Conservative 51; Mismatches 54; Indels 4; Gaps 2;

QY 1 MVMNFKVFKKCAPNGKVTLYMGKRDVHVSGVEPIDGIIVLDDXEYIRDNKRVFGQIVCS 60
DB 1 MVMNFKVFKKCAPNGKVTLYMGKRDVHVSGVEPIDGIIVLDDXEYIRDNKRVFGQIVCS 60
QY 61 FRYGREDEVMGLNFQKELCLASEQIYRPREKSDKEQTKLQERLLKLGSNALPFTFNIS 120
DB 61 FRYGREDEVMGLNFQKELCLASEQIYRPREKSDKEQTKLQERLLKLGSNALPFTFNIS 120
QY 121 PNAPSSVTLOQGEDDNGDPGCVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQCG 180
DB 121 PNAPSSVTLOQGEDDNGDPGCVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQCG 180
QY 181 QPCTLVKRDFMLSPGELLEVTLTKQLYHGERIGVNICIRNNSNMKVKKIKAMVOQGV 240
DB 181 QPCTLVKRDFMLSPGELLEVTLTKQLYHGERIGVNICIRNNSNMKVKKIKAMVOQGV 240
QY 241 VVLPQNGSYRNTVASLETSEGCPIQPGSSLOKVMYLTPLSSNKQRRGIALDGOIKRQDQ 300
DB 241 VVLPQNGSYRNTVASLETSEGCPIQPGSSLOKVMYLTPLSSNKQRRGIALDGOIKRQDQ 300
QY 301 CLASTTLLAQPDQDAFGVIISYAVKVKLFLGALGGELSAELPFVLMHPKPGTKAKVIHA 360
DB 301 CLASTTLLAQPDQDAFGVIISYAVKVKLFLGALGGELSAELPFVLMHPKPGTKAKVIHA 360
QY 361 DSQADVE 367
DB 361 DSQADVE 367

RESULT 4
ADQ89588 standard; protein; 364 AA.
ID ADQ89588
XX ADQ89588,
AC ADQ89588,

XX 21-OCT-2004 (first entry)
DT
XX Antagonist of cell cycle progression polypeptide #9.
DE
XX
XX Cytostatic; cancer; cell division cycle; mitosis; meiosis;
KW cell cycle progression.
XX
XX Drosophila melanogaster.
OS
XX
XX WO2004063362-A2.
PN
XX
XX 29-JUL-2004.
PD
XX
XX 31-DEC-2003; 2003WO-GB005635.
PF
XX
XX 10-JAN-2003; 2003US-0439123P.
PR 06-MAY-2003; 2003US-0468402P.
XX
XX (CYCL-) CYCLACEL LTD.
PA
XX
XX Glover D, Bell G, Frenz L, Midgley C;
PI
XX WPI; 2004-544089/52.
DR N-PSDB; ADQ89587.
XX
XX New cell cycle progression genes and proteins for modulating cell cycle
PT progression in cells, for preventing, treating or diagnosing cell
PT proliferative diseases (e.g. cancer) or for identifying modulators of
PT mitosis or meiosis.
XX
XX
PS Claim 2; SEQ ID NO 18; 461pp; English.
XX
XX The present invention relates to a polynucleotide for preventing,
CC treating or diagnosing a disease in an individual. The composition or the
CC polypeptide, polynucleotide or RNA precursor, or antibody is useful for
CC diagnosing, preventing or treating diseases (e.g. cell proliferative
CC diseases such as cancer) in an individual. These may also be used for
CC identifying substances capable of binding to or modulating the function
CC of the polypeptide, capable of affecting the function of the
CC corresponding gene, or capable of inhibiting the cell division cycle or
CC cell cycle progression, preferably mitosis and/or meiosis. The present
CC sequence represents an antagonist of cell cycle progression protein
XX
XX Sequence 364 AA;

Query Match 70.1%; Score 1384; DB 8; Length 364;
Best Local Similarity 70.3%; Pred. No. 1.5e-135;
Matches 258; Conservative 51; Mismatches 54; Indels 4; Gaps 2;

QY 1 MVMNFKVFKKCAPNGKVTLYMGKRDVHVSGVEPIDGIIVLDDXEYIRDNKRVFGQIVCS 60
DB 1 MVMNFKVFKKCAPNGKVTLYMGKRDVHVSGVEPIDGIIVLDDXEYIRDNKRVFGQIVCS 60
QY 61 FRYGREDEVMGLNFQKELCLASEQIYRPREKSDKEQTKLQERLLKLGSNALPFTFNIS 120
DB 61 FRYGREDEVMGLNFQKELCLASEQIYRPREKSDKEQTKLQERLLKLGSNALPFTFNIS 120
QY 121 PNAPSSVTLOQGEDDNGDPGCVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQCG 180
DB 121 PNAPSSVTLOQGEDDNGDPGCVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQCG 180
QY 181 QPCTLVKRDFMLSPGELLEVTLTKQLYHGERIGVNICIRNNSNMKVKKIKAMVOQGV 240
DB 181 QPCTLVKRDFMLSPGELLEVTLTKQLYHGERIGVNICIRNNSNMKVKKIKAMVOQGV 240
QY 241 VVLPQNGSYRNTVASLETSEGCPIQPGSSLOKVMYLTPLSSNKQRRGIALDGOIKRQDQ 300
DB 241 VVLPQNGSYRNTVASLETSEGCPIQPGSSLOKVMYLTPLSSNKQRRGIALDGOIKRQDQ 300
QY 301 CLASTTLLAQPDQDAFGVIISYAVKVKLFLGALGGELSAELPFVLMHPKPGTKAKVIHA 360
DB 301 CLASTTLLAQPDQDAFGVIISYAVKVKLFLGALGGELSAELPFVLMHPKPGTKAKVIHA 360

Db 300 ALASTTLIASQDARDAPGIIIVSAVKVFLGALGELCAELPFIIMHPKPSRKAQL--- 356
 QY 361 DSQADVE 367
 Db 357 BAEGSIE 363

RESULT 5
 ABR844484
 ID ABR844484 standard; protein; 398 AA.
 AC ABR844484;
 XX
 DT 15-JAN-2004 (first entry)
 DE Mosquito olfaction molecule, arrestin 2.
 KW Arrestin 2; mosquito; olfaction; insecticide; antimalarial.
 OS Anopheles gambiae.
 XX
 FH Key
 FT Misc-difference 152
 FT /note= "Encoded by AG"
 XX
 PN WO2003076590-A2.
 XX
 PD 18-SEP-2003.
 XX
 PF 10-MAR-2003; 2003WO-US007174.
 XX
 PR 08-MAR-2002; 2002US-00094240.
 XX
 PA (UYVA-) UNIV VANDERBILT.
 XX
 PI Zwiebel LJ;
 XX
 DR WPI; 2003-722331/68.
 DR N-PSDB; ACF79731.
 XX
 PT New mosquito arrestin 1 and 2 genes and polypeptides, useful for
 PT identifying mosquito olfaction molecule binding compounds which reduce
 PT the ability of mosquitoes to locate sources of bloodmeal, e.g. humans.
 PS Claim 16; Fig 12b; 101bp; English.
 XX
 CC The present sequence is the protein sequence of arrestin 2, a novel
 CC mosquito olfaction molecule. The invention provides 9 novel mosquito
 CC polypeptides and the nucleic acids encoding them. These are arrestins 1
 CC and 2 and odorant receptor molecules 1-7. The odorant receptor 1
 CC in a ligand-induced signal transduction pathway for the activation of
 CC mosquito olfaction. Arrestin functions to inhibit the activation of
 CC transduction cascade. Thus, the odorant receptors act as an 'on' switch
 CC and arrestin as an 'off' switch for the odorant detection system of the
 CC mosquito. Methods are provided for identifying compounds that interfere
 CC with the operation of the mosquito olfactory system, particularly
 CC compounds that modulate arrestin 2 activity. These are useful for the
 CC control of mosquitoes, particularly by reducing their ability to locate
 CC sources of bloodmeal.
 XX
 SQ Sequence 398 AA;

Query Match
 Best Local Similarity 51.8%; Score 1023; DB 7; Length 398;
 Matches 204; Conservative 65; Mismatches 111; Indels 10; Gaps 7;
 QY 1 MYTNFKVFKKCAPNGKVTLYMGKRDVHVSVEPIDGIVLDEYIRDNRYVGGQIVCS 60
 Db 1 MYVAVKVFKKSAPNGKLTLYLGKRDVIDHTYCDPIDGVIVLDEEYLR-GRKVFGLITTT 59
 QY 61 FRYGREDEBVMGLNFQKELCLASFOIYPRPEKSDKEQTKLOERLJKLTGSNAIPTFNIS 120
 Db 60 YRYGREDEBVMGVKFSKEMVLTKEQIYPM-ENANMEMTPMOERLVKLTGANAFPFTHFP 118

QY 121 PNPSSVTLQOGEDNDGDCGVSYVYKIFAGESETDTRHRSVTTLGIRKIQFAPTKOQ 180
 Db 119 SMAPSSVTLQAGEDDTGKPLGVEYAIKAHVGEDESDKGHRSAVTLTIKKLQYAPVSRGR 178
 QY 181 Q-PCITLVKDFMLSPGELELEVTDKQLYLHGERIGVNICIRNNSKMKVKIKAMVQGV 239
 Db 179 RLPSSLVSKGFTFSQCKINLEVTLDREIYHGEKIANIVTNSRKTVKSIKCFVQHC 238
 QY 240 DVVLFQNGSYRNTVYASLETSGCPIDPGSSLQKVMYLTPLSSNKORGIALDGQIKRQD 299
 Db 239 EVTMV-NAQFSKHIALSELTREGCPIFGASFTKSPFLVPLASSNCKDRGIALDGHKEED 297
 QY 300 QCLASTTLIAQPD-QRDAFGVVISYAVKVKLFLGALGGEISAEIPFVLMHPKPGT--KAK 356
 Db 298 VNLAASSTLISEGKCPSPDAMGIVTISLRVKNCGTLGGLQTDVPEPKLMNPAPGVERER 357
 QY 357 VTHADSQADVETFRQDT--IDQASVDPE 383
 Db 358 VNALKKMSIERHRYENSHYADDNDNIVFE 387

RESULT 6
 ABB58174
 ID ABB58174 standard; protein; 470 AA.
 AC ABB58174;
 XX
 DT 26-MAR-2002 (first entry)
 DE Drosophila melanogaster polypeptide SEQ ID NO 1314.
 XX
 KW Drosophila; developmental biology; cell signaling; insecticide;
 KW pharmaceutical.
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US009231.
 XX
 PR 23-MAR-2000; 2000US-0191637P.
 PR 11-JUL-2000; 2000US-00614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW,
 DR WPI; 2001-656860/75.
 DR N-PSDB; ABL02277.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signaling and cell-cell
 PT interactions.
 PS Disclosure; SEQ ID NO 1314; 21bp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signaling and
 CC cell-cell interactions in higher eukaryotes for the development and
 CC insecticides, therapeutics and pharmaceutical drugs. The invention of
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
 CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 470 AA;

Query Match
 50.8%; Score 1002; DB 4, Length 470,

Best Local Similarity 53.7%; Pred. No. 2.4e-95;
Matches 187; Conservative 70; Mismatches 87; Indels 4; Gaps 3;
QY 6 KVFKKCAPNGKVTLYMGKDFVDHVSVEPIDGIVLDEYIRDNRKVFQIVCSFRYGR 65
DB 48 RVFKKSSNGKITVYLKGRDFVDHVTHTVDIDGVFIDPEYVKD-RKVFQVLAAFRYGR 106
QY 66 EDEVMGLNFQKELCLASEQIYRPREKSDKEQTKLQERLLKLGSNAIPTFNISPNAPS 125
DB 107 EDLDVLGLTFRKDLVLAHQIYR-PMQLDRPMTRLQERLLKLGPNHHPYFEVPPYCPA 165
QY 126 SVTLQOGEDDNGDPCGVSYYVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQOQCTL 185
DB 166 SVSLQAPAGDVGKSCGVDEYELKAFVGENVEDKPKRNSVRLTIRKVMYAPSKVGEQPSIE 225
QY 186 VRKDFMLSPGELEVTLDKQLYLHGERIGVNICIRNNSNKKVKKIKAMVOQGVDFVLFQ 245
DB 226 VSKFPMKPKNIHLKATLDLDELHNGEKISVNVHANNSTRTVKIKVCFVQFADICLFS 285
QY 246 NGSYRNTVASLETSEGCPIQPGSSLOKVMYLTPLSSNKGORGIALDGOIKRQDQCLAST 305
DB 286 TAQYKSVVAEIESEDGCVAPGFTLSKVFEIPLANNKDKWGLALDGLKHEDTNLASS 345
QY 306 TLLAOPDQDAFGVIISYAVKYLFLGA--LGELSAELPFVLMHPKP 351
DB 346 TLITNPAQRESLIGIMVHYKVKVLLISSPLNGDLVAELPFTLMHPKP 393
RESULT 7
ABB61964
ID ABB61964 standard; protein; 401 AA.
XX ABB61964;
XX 26-MAR-2002 (first entry)
XX Drosophila melanogaster polypeptide SEQ ID NO 12684.
DE Drosophila melanogaster polypeptide SEQ ID NO 12684.
XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX Drosophila melanogaster.
OS WO200171042-A2.
XX
PN 27-SEP-2001.
PD 23-MAR-2001; 2001WO-US009231.
PE 23-MAR-2001; 2000US-0191637P.
PR 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
PA (PEKE) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
PI
XX
XX WPI; 2001-656860/75.
DR N-PSDB; ABL06067.
DR
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions.
XX
XX
PS Disclosure; SEQ ID NO 12684; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the

CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 401 AA;
QY Query Match 49.8%; Score 982.5; DB 4; Length 401;
Best Local Similarity 48.7%; Pred. No. 2.1e-93;
Matches 191; Conservative 73; Mismatches 115; Indels 13; Gaps 6;
QY 1 MVTNFKYFKKCAPNGKVTLYMGKDFVDHVSVEPIDGIVLDEYIRDNRKVFQIVCS 60
DB 1 MVSVKYFKKATPNGKVFYLLGRDRFDIHDYCDPVDGVIVVEPDYLR-NRKVFQQLATT 59
QY 61 FRYGREDEVMGLNFQKELCLASEQIYRPREKSDKEQTKLQERLLKLGSNAIPTFNIS 120
DB 60 YRYGREDEVMGVKFSKELILCREQIVPN-TNPNMEMTPWQEKLVKLGSNAYPTFHP 118
QY 121 PNAPSSVTLQOGEDDNGDPCGVSYYVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQG 180
DB 119 PNPSSVTLQOGEDDNGKPLGVEYTIIRAFVGDSEDDRQHRSMVSLVIRKLQYAPLRGQ 178
QY 181 Q-PCTLVKDFMLSPGELEVTLDKQLYLHGERIGVNICIRNNSNKKVKKIKAMVOQGV 239
DB 179 RLPSSLSKGFTFNSNGKISLEVTLDREIYHGEKTAATVQVSNSSKSVSIKCFIVQHT 238
QY 240 DVLVFNQGSYRNTVASLETSEGCPIQPGSSLOKVMYLTPLSSNKGORGIALDGOIKRQ 299
DB 239 EITMV-NAQFSKHVAQLTEKEGCPITPGANLTFTFYLLPLAANNKDRHGIALDGLKDED 297
QY 300 QCLASTLLAQ-PDQDAFGVIISYAVKYLFLGALGELSAELPFVLMHPKPPT----- 353
DB 298 VNLASTTWQEGKSTGDACGIVISYSVRKILNCGTLGEMQTDVPFKLQAPAGTIEKR 357
QY 354 ---KAKVIHADSQADVETFRQDTIDQASVDF 382
DB 358 SNAMKKMKSIEQHRNVKGYQQDDDDNIVEEDF 389
RESULT 8
AAG67780
ID AAG67780 standard; protein; 410 AA.
XX
AC AAG67780;
XX
DT 10-DEC-2001 (first entry)
XX
DE Amino acid sequence of human beta-arrestin 1B.
XX
KW Arrestin; phosphorylation-independent arrestin mutant;
KW G protein-coupled receptor; GPCR; GPCR ligand; retinitis pigmentosa;
KW stationary night blindness; colour blindness; nephrogenic DI;
KW isolated glucocorticoid deficiency; hyperfunctioning thyroid adenoma;
KW familial hypocalcaemic hypercalcaemia; hyperparathyroidism;
KW neurological disorder.
XX
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT Region 155..184
FT /note= "putative phosphorylation-recognition region"
XX
PN WO200167106-A2.
PD 13-SEP-2001.
PD
XX
PF 05-MAR-2001; 2001WO-US007304.
PF
XX
PR 03-MAR-2000; 2000US-0186706P.
PR
XX (MILL-) MILLENNIUM PHARM INC.
PA
XX
PI Bernstein G;
XX

DR WPI, 2001-602637/68.

XX Identifying a G protein-coupled receptor ligand, useful for treating e.g.
PT retinitis pigmentosa, color blindness or neurological disorders, uses
PT phosphorylation-independent arrestin mutants particularly suited for in
XX vitro screening assays.

XX Disclosure; Page 46; 47pp; English.

XX The present sequence represents an arrestin protein. The specification
CC describes phosphorylation-independent arrestin mutants. These mutants are
CC used in screening assays to identify ligands and/or modulators of G
CC protein-coupled receptors (GPCRs). A method for identifying a GPCR ligand
CC comprises contacting a composition comprising the GPCR and a
CC constitutively active arrestin mutant with a test compound; and
CC determining the ability of the test compound to modulate binding of
CC arrestin mutant to the GPCR, where modulation of binding indicates that
CC the test compound is a GPCR ligand. The method is used for identifying
CC potential ligands and/or modulators of GPCRs, particularly modulators
CC for use as human therapeutics. Modulators of GPCR may be used for
CC treating patients having e.g. retinitis pigmentosa, stationary night
CC blindness, colour blindness, nephrogenic DI, isolated glucocorticoid
CC deficiency, hyperparathyroidism and neurological disorders. The
CC hypercalcemia, hyperparathyroidism and neurological disorders. The
CC methods may be used for screening pluralities of test compounds (e.g. a
CC small molecule library of compounds) or a composition containing a
CC plurality of GPCRs. The methods may be used in screening assays for
CC identification of natural and surrogate agonists of orphan GPCRs, and for
CC identification of GPCR antagonists and/or agonists

XX Sequence 410 AA;

Query Match
Best Local Similarity 46.0%; Score 907.5; DB 4; Length 410;
Matches 176; Conservative 78; Mismatches 112; Indels 7; Gaps 4;

QY 6 KVEKCCAPNGKVTLYMGKRDVFDVHSGVEPIDGIVLDEYIRDNKRVGQIVCSFRYGR 65
DB 7 RVFKKASPNKLTIVLIGKRDVFDHIDLVDVGVLDPEYLKE-RRVYVTLTCAFRYGR 65
QY 66 EDEVMGILNFOKELCLASEQIYPRPEKSDKEQTKLOERLLKLGSNAPFTFNISPNAPS 65
DB 66 EDLDVLGLTFRKDLFVANVQSFPPAPEDKKPLTRLQERLIKLGHAHYPTFEIPNLPC 125
QY 126 SVTLQOGEEDNDGDCGVSYYVKIFAGSEETDRTHRSVTTLGIRKIQAPRTKQGOQPCTL 125
DB 126 SVTLQOGEEDNDGDCGVSYYVKIFAGSEETDRTHRSVTTLGIRKIQAPRTKQGOQPCTL 185
QY 186 VRKDFMLSPGELEVTLDKQLYHGERIGVNICIRNNSNMVKIKRAMVQGOQDVVLFQ 185
DB 186 TTRQFLMSDKPLHLERASLDKEIYHGEPISVNVTNNTKTVKKIKISVQYADICLEN 245
QY 246 NGSYRNTVASLETSEGCPIQPGSSLOKVMYLTPLSSNKQRGIALDGOIKRQDQCLAST 245
DB 246 TAQYKCPVAMEADD--TVAPSSTFCKVYTLTPTLANNREKRGIALDQKLEHEDTNLASS 303
QY 306 TLLAQPDQDADFVGIISYAVKVLFTLGLGELSAELPFVLMHPKPGTK--AKVIHADS 303
DB 304 TLLREGANREILGIVSYKVKVL-VESRGGDVAVELPFTLMHPKKEEPPHREVEENET 362
QY 363 QADVETFRQDTID 375
DB 363 PVDTNLIEDTND 375

RESULT 9
ID AAG67778 standard; protein; 418 AA.
XX AAG67778;
AC AAG67778;
XX 10-DEC-2001 (first entry)
DT
XX

DE Amino acid sequence of bovine beta-arrestin 1A.
XX
XX Arrestin; phosphorylation-independent arrestin mutant;
KW G protein-coupled receptor; GPCR; GPCR ligand; retinitis pigmentosa;
KW stationary night blindness; colour blindness; nephrogenic DI;
KW isolated glucocorticoid deficiency; hyperfunctioning thyroid adenoma;
KW familial hypocalcemic hypercalcemia; hyperparathyroidism;
KW neurological disorder.
XX
XX Bos sp.

OS
FH Key
FT Region
FT .184
XX Location/Qualifiers
XX /note="putative phosphorylation-recognition region"

PN WO200167106-A2.
XX
XX 13-SEP-2001.

PP 05-MAR-2001; 2001WO-US007304.

PR 03-MAR-2000; 2000US-0186706P.

PA (MILL-) MILLENNIUM PHARM INC.

PI Berstein G;

DR WPI, 2001-602637/68.

XX Identifying a G protein-coupled receptor ligand, useful for treating e.g.
XX retinitis pigmentosa, color blindness or neurological disorders, uses
XX phosphorylation-independent arrestin mutants particularly suited for in
XX vitro screening assays.

XX Disclosure; Page 46; 47pp; English.

XX The present sequence represents an arrestin protein. The specification
CC describes phosphorylation-independent arrestin mutants. These mutants are
CC used in screening assays to identify ligands and/or modulators of G
CC protein-coupled receptors (GPCRs). A method for identifying a GPCR ligand
CC comprises contacting a composition comprising the GPCR and a
CC constitutively active arrestin mutant with a test compound; and
CC determining the ability of the test compound to modulate binding of
CC arrestin mutant to the GPCR, where modulation of binding indicates that
CC the test compound is a GPCR ligand. The method is used for identifying
CC potential ligands and/or modulators of GPCRs, particularly modulators
CC for use as human therapeutics. Modulators of GPCR may be used for
CC treating patients having e.g. retinitis pigmentosa, stationary night
CC blindness, colour blindness, nephrogenic DI, isolated glucocorticoid
CC deficiency, hyperparathyroidism and neurological disorders. The
CC hypercalcemia, hyperparathyroidism and neurological disorders. The
CC methods may be used for screening pluralities of test compounds (e.g. a
CC small molecule library of compounds) or a composition containing a
CC plurality of GPCRs. The methods may be used in screening assays for
CC identification of natural and surrogate agonists of orphan GPCRs, and for
CC identification of GPCR antagonists and/or agonists

XX Sequence 418 AA;

Query Match
Best Local Similarity 45.8%; Score 903.5; DB 4; Length 418;
Matches 179; Conservative 76; Mismatches 112; Indels 13; Gaps 5;

QY 6 KVEKCCAPNGKVTLYMGKRDVFDVHSGVEPIDGIVLDEYIRDNKRVGQIVCSFRYGR 65
DB 7 RVFKKASPNKLTIVLIGKRDVFDHIDLVDVGVLDPEYLKE-RRVYVTLTCAFRYGR 65
QY 66 EDEVMGILNFOKELCLASEQIYPRPEKSDKEQTKLOERLLKLGSNAPFTFNISPNAPS 65
DB 66 EDLDVLGLTFRKDLFVANVQSFPPAPEDKKPLTRLQERLIKLGHAHYPTFEIPNLPC 125
QY 126 SVTLQOGEEDNDGDCGVSYYVKIFAGSEETDRTHRSVTTLGIRKIQAPRTKQGOQPCTL 185

DB 126 SVTLQGPEDTGKACGVDEYVKAFC AENLEEKIHKNSVRLVIRKQVAPBRGPQTAE 185
QY 186 VRKDFMLSPGELELEVTLDKQLYLHGERIGVNICIRNNSNMVKIKAMVQGVDFVLFQ 245
DB 186 TTRQFLMSDKPRLHLEASLDKEIYYHGEPISVNVHTNNTKTVKKIKISVQYADICLFN 245
QY 246 NGSYRNTVASLETSEGCPIQPGSSLOKVMYLTPLSSNKQRGIALFGQIKRQDQCLAST 305
DB 246 TAQYKCPVAMEEADD--TVAPSSTFCKVYTLTPFLANNREKRGALDGKHKHEDTNLAAS 303
QY 306 TLLAQPDQRDAFGVIISYAVKVKLFL--GALGGLSA-----ELPFVLMHPKPGTK---A 355
DB 304 TLLREGANREILGIIVSYKVKVCLVSRGGLGLDASSDVAVELPFTLMHPKPKKEPPHR 363
QY 356 KVIHADSQADVETFRQDTID 375
DB 364 EVPEHETPVDTNLIELDTND 383
RESULT 10
ABG69495
ID ABG69495 standard; protein; 452 AA.
XX AC ABG69495;
XX DT 21-OCT-2002 (first entry)
XX DE Rat bait protein beta arrestin 1.
XX KW Rat; Yeast two-hybrid assay; adipocyte; bait protein; NIDDM;
KW non-insulin diabetes mellitus; obesity; selected interacting domain; SID;
KW protein-protein interaction map; PIM; anorectic; metabolic disorder.
XX OS Rattus sp.
XX PN WO200253726-A2.
XX PD 11-JUL-2002.
XX PF 28-DEC-2001; 2001WO-EP015423.
XX PR 02-JAN-2001; 2001US-0259377P.
XX PA (HYBR-) HYBRIGENICS.
XX PA (CNRS) CENT NAT RECH SCI.
XX PI Legrain P, Marullo S, Jockers R;
XX PI WPI; 2002-583612/62.
XX DR N-PSDB; ABS51031.
XX PT Novel complex of protein-protein interactions in adipocyte cells for
PT identifying compounds that modulate the protein-protein interactions and
PT useful for treating obesity and metabolic disorders.
XX PS Claim 1; Page 52; 125pp; English.
XX CC The invention relates to a complex of protein-protein interactions
CC (forming a protein-protein interaction map, PIM) in adipocyte cells as
CC defined in the specification, or polynucleotides in adipocytes encoding
CC for the polypeptides. Also included are a recombinant cell expressing the
CC interacting polypeptides and a method of selecting a modulating compound
CC in adipocyte cells, by cultivating a recombinant host cell on a selective
CC medium containing a modulating compound and a reporter gene the
CC expression of which is toxic for the recombinant host cell which is
CC transformed with two vectors, where the first vector comprises a
CC polynucleotide encoding a first hybrid polypeptide and DNA binding domain
CC and the second vector comprising a polynucleotide encoding a second
CC hybrid polypeptide and an activating domain that activates the toxic
CC reporter gene, when the first and second hybrid polypeptides interact and
CC selecting the modulating compound which inhibits the growth of the
CC recombinant host cell (i.e. using the yeast two-hybrid system). The
CC complexes are useful for identifying compounds that modulate the protein-

CC protein interactions and useful for treating obesity and metabolic
CC disorders e.g. non-insulin dependent diabetes mellitus, NIDDM. The
CC compound isolated by the method is useful for treating and preventing
CC obesity or metabolic diseases. The interactions between the proteins of
CC the complex further define a set of selected interacting domains, SID.
CC The present sequence represents a member of the protein complex of the
CC invention, used as the bait protein in the yeast two- hybrid assay
XX SQ Sequence 452 AA;
Query Match 45.8%; Score 903.5; DB 5; Length 452;
Best Local Similarity 47.1%; Pred. No. 4.7e-85;
Matches 179; Conservative 76; Mismatches 112; Indels 13; Gaps 5;
QY 6 KVFKKCAPNGKVTLYMGKRD FVDHVS GVEPI DIGIVL DDEYIRDN RKVGOIVCSFRYGR 65
DB 7 RVFKKASPNGKLT VYLGKRD FVDHIDLVEPVDGV LVDP EYLKE-RRVYVTLTCAFRYGR 65
QY 66 EDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLOERLLKLGSMNAPPTFNISPNAPS 125
DB 66 EDDLVLGLTFRKDLFVAVNVQSFPPAPEDKKPLTRLQERLIKLG EHAHYFTFEIIPNLP 125
QY 126 SVTLQGEDDNDGDPGCVSYVKIFAGSESDTRTHRSTVTLGIRKIQFAPTKOGQOQPTL 185
DB 126 SVTLQGPEDTGKACGVDEYVKAFC AENLEEKIHKNSVRLVIRKQVAPBRGPQTAE 185
QY 186 VRKDFMLSPGELELEVTLDKQLYLHGERIGVNICIRNNSNMVKIKAMVQGVDFVLFQ 245
DB 186 TTRQFLMSDKPRLHLEASLDKEIYYHGEPISVNVHTNNTKTVKKIKISVQYADICLFN 245
QY 246 NGSYRNTVASLETSEGCPIQPGSSLOKVMYLTPLSSNKQRGIALFGQIKRQDQCLAST 305
DB 246 TAQYKCPVAMEEADD--TVAPSSTFCKVYTLTPFLANNREKRGALDGKHKHEDTNLAAS 303
QY 306 TLLAQPDQRDAFGVIISYAVKVKLFL--GALGGLSA-----ELPFVLMHPKPGTK---A 355
DB 304 TLLREGANREILGIIVSYKVKVCLVSRGGLGLDASSDVAVELPFTLMHPKPKKEPPHR 363
QY 356 KVIHADSQADVETFRQDTID 375
DB 364 EVPEHETPVDTNLIELDTND 383
RESULT 11
ABG70174
ID ABG70174 standard; protein; 418 AA.
XX AC ABG70174;
XX DT 21-OCT-2002 (first entry)
XX DE Human prey protein for Shigella ipan9.8 #4.
XX KW Prey protein; ospB; ospD; ipad; ipac; ipan9.8; ospG; ospC1; Shigella;
KW shigellosis; bacillary dysentery; antibacterial; yeast two-hybrid system;
KW protein-protein interaction; SID; selected interacting domain; human.
XX OS Homo sapiens.
XX PN WO200257303-A2.
XX PD 25-JUL-2002.
XX PF 11-JAN-2002; 2002WO-EP000777.
XX PR 12-JAN-2001; 2001US-0261130P.
XX PA (HYBR-) HYBRIGENICS.
XX PI Legrain P;
XX DR WPI; 2002-599706/64.
DR N-PSDB; ABS51567.

XX New complex of protein-protein interactions between a bait Shigella
PT flexneri polypeptide and a prey mammalian or human placenta polypeptide
PT for treating or preventing bacillary dysentery in a mammal or human.
PT
XX
PS Claim 7; Page 117-118; 162pp; English.
CC The invention.

CC The invention relates to a complex of protein-protein interactions
 CC between a Shigella flexneri polypeptide (e.g. ospB, ospD, ipad, ipac,
 CC ipah9.8, ospg and ospC1) and a mammalian polypeptide defined in the
 CC specification. The complexes are formed using the polypeptide defined in the
 CC system. Also included are (1) a recombinant host cell expressing the
 CC interactions between the Shigella flexneri polypeptide and a mammalian
 CC polypeptide defined in the specification; (2) selecting a modulating
 CC compound that inhibits or activates the protein-protein interactions;
 CC (selected interacting compound obtained from the method of (2); (4) a SID
 CC comprising the human polypeptides appearing or its fragment or variant
 CC SID polynucleotide or its fragment comprising as ABG70042-ABG70242; (5) a
 CC above polypeptides a vector comprising (5); (6) a recombinant host cell
 CC containing the vector; and (10) a protein chip comprising Shigella
 CC flexneri polypeptide and a mammalian polypeptide defined in the
 CC specification. A pharmaceutical composition comprising Shigella
 CC polypeptide or polynucleotide is useful for treating or preventing
 CC shigellosis (bacterial dysentery) in a human or mammal. The present
 CC sequence represents a human prey protein isolated by the yeast two-hybrid
 CC assay, forming a complex of the invention with a shigella protein
 CC
 CC Sequence 418 AA;

Query Match	45.6%;	Score 900.5;	DB 5;	Length 418;
Best Local Similarity	46.8%;	Pred. No. 8.6e-85;		
Matches 178;	Conservative 77.			

QY	6	KVEKKCAPNGKVTLYMGKRD	FVDVHVS	GVEPIDGIVL	DDXEYIR	DNKRYFGQIVCS	FERYGR	65	
Db	7	RVFKKASPNGLT	VYLGKRD	FVHDH	LDVDP	VGVVLVD	PEYLKE	-R	VYVTLTCAFRYGR
QY	66	EEDVWMGINF	OKELCL	ASEQIVR	PEKSD	EQTKLOERLLK	KTLSNAIP	FTFNIS	PNABS
Db	66	EDLDVLGL	TRFKDLF	VANVOS	FP	PAPAD	EKKPLTRLOER	LTKLGE	HAYFTFEI
QY	126	SVTLQOGEDD	NDPCGV	SYVVKI	PAGESET	DRTHR	STVTYL	GIRKI	QFAP
Db	126	SVTLQGPEDT	GKACGV	YEVKAF	CAENLE	EKKIKH	RNSV	ALVIR	KQYAP
QY	186	VRKDFMLSP	GEELE	VTLDK	OLYL	GERIG	VNICIR	NNSN	KMVKKT
Db	186	TTROFLMS	DKPLH	LEAS	LDKEI	TYHGE	PISV	NVHVT	NNNTK
QY	246	NGSYNTV	ASLET	SEGCPI	QPGSSL	OKWYL	TP	PLT	SSNK
Db	246	TAYQKCP	VAME	EADD	-T	VAP	STF	ECVY	TLT
QY	306	TLIAQPD	QRDA	FGVIT	ISAV	KVKFL	-G	ALG	ELSA
Db	304	TLTREGAN	REI	LGIT	IVSY	KVKAL	VSR	GG	LLGL
QY	356	KVIHAD	SQAD	VETFR	RODTID	375			
Db	364	EVPENET	PVD	TN	LI	ELD	TND	383	

RESULT 12	
ADQ89786	
ID	ADQ89786 standard; protein; 418 AA
XX	
AC	ADQ89786;
XX	
DT	21-OCT-2004 (first entry)
XX	
DE	Antagonist of cell cycle progression
XX	

KW Cytostatic; cancer; cell division cycle; mitosis; meiosis
KW cell cycle progression.
XX

New cell cycle progression genes and proteins for modulating cell cycle progression in cells, for preventing, treating or diagnosing cell cycle proliferative diseases (e.g. cancer) or for identifying cell cycle mitosis or meiosis.

Claim 2; SEQ ID NO 216; 461bp; English.

CC... of diagnosing a disease in an individual. The composition or the
CC polypeptide, polynucleotide or RNA precursor, or antibody is useful for
CC diagnosing, preventing or treating diseases (e.g. cell proliferative
CC diseases such as cancer) in an individual. These may also be used for
CC identifying substances capable of binding to or modulating the function
CC of the polypeptide, capable of affecting the function of the
CC corresponding gene, or capable of inhibiting the cell division cycle or
CC cell cycle progression, preferably mitosis and/or meiosis. The present
CC sequence represents an antagonist of cell cycle progression protein
XX
SQ Sequence 418 AA;

Query Match	45.6%	Score 900.5	DB 8	Length 418
Best Local Similarity	46.8%	Pred. No. 8.6e-85		
Matches 178	Conservative 77	Mismatches 112	Indels 13	Gaps 5
QY	6	KVFKKCAPNGKVTLLYMGKRDVFDVHVSQVEPLDGIWLDDEYIRDNKRYFGQIVCSFRYGR	65	
DB	7	RVEKKASPNGLTIVYLGKRDVFDHIDLVDVVDGVLVDPEYLKE-RRVYVTLTCAFRYGR	65	
QY	66	EEDVWGLNFQKELCLASEQIYRPRPEKSDKEQTKQERLLKGLSNAIFPTNPISPMAPS	125	
DB	66	EDLDVLGLTFRKDLFVANQSPFPAPBEDKKPLTLRQERLIKGLGEHAYPTFEIPNLPC	125	
QY	126	SVTLQGGEDDNGDPCGVSYVVKIPAGESETDRTHRSTVTLGIRKIQAPTKOGQOQPTL	185	
DB	126	SVTLQPGPEDTGKACGVDEYVKAFCALNLEKIKHRNSVRLVIRKQYAPERPCQPATAE	185	
QY	186	VRKDFMLSPGELFVTLDKOLYLHGERIGVNICIRNNSNMKVKKIKAMVQGVDPVTLFQ	245	
DB	186	TTRQFLMSDKPLHLIASLDEIKIYYHGEPISVNHVNTNTNKTKKIKISVRQYADICLFN	245	
QY	246	NGSVRNTVASLETSSEGCPIQPGSSLOKMYLTPRLISSNKORGIALDGQIKRQDQCLAST	305	
DB	246	TAYQKCPVAMEEADD--TVAPSSTFCKVYTLTPFLANNREKRGALDGLKHEIDTNLAASS	303	
QY	306	TLLAQPDQDAFGVITISYAVKYLFL--GALGELSA-----ELPEVLMHPKPGTK---A	355	
DB	304	TLLREGANREITLGIIVSYKVKIKLTVSRGGLLGLDIASSDVAVELPFTLTHPKPKKEP	363	
QY	356	KVIHADQADVETFRQDTTD	375	
DB	364	EVPENETPVDTNLTIELDTND	383	

RESULT 13
AAG67779
ID AAG67779 standard; protein; 418 AA.
XX
AC AAG67779;
XX
DT 10-DEC-2001 (first entry)
XX
DE Amino acid sequence of human beta-arrestin 1A.
XX
KW Arrestin; phosphorylation-independent arrestin mutant;
KW G protein-coupled receptor; GPCR; GPCR ligand; retinitis pigmentosa;
KW stationary night blindness; colour blindness; nephrogenic DI;
KW isolated glucocorticoid deficiency; hyperfunctioning thyroid adenoma;
KW familial hypocalciuric hypercalcaemia; hyperparathyroidism;
KW neurological disorder.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 155..184
PT /note= "putative phosphorylation-recognition region"
XX
PN WO200167106-A2.
XX
PD 13-SEP-2001.
XX
PF 05-MAR-2001; 2001WO-US007304.
XX
PR 03-MAR-2000; 2000US-0186706P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Berstein G;
XX
DR WPI; 2001-602637/68.
XX
PT Identifying a G protein-coupled receptor ligand, useful for treating e.g.
PT retinitis pigmentosa, color blindness or neurological disorders, uses
PT phosphorylation-independent arrestin mutants particularly suited for in
PT vitro screening assays.
XX
XX
XX Disclosure; Page 46; 47pp; English.
PS
XX
XX The present sequence represents an arrestin protein. The specification
CC describes phosphorylation-independent arrestin mutants. These mutants are
CC used in screening assays to identify ligands and/or modulators of G
CC protein-coupled receptors (GPCRs). A method for identifying a GPCR ligand
CC comprises contacting a composition comprising the GPCR and a
CC constitutively active arrestin mutant with a test compound; and
CC determining the ability of the test compound to modulate binding of
CC arrestin mutant to the GPCR, where modulation of binding indicates that
CC the test compound is a GPCR ligand. The method is used for identifying
CC potential ligands and/or modulators of GPCRs, particularly modulators,
CC for use as human therapeutics. Modulators of GPCR may be used for
CC treating patients having e.g. retinitis pigmentosa, stationary night
CC blindness, colour blindness, nephrogenic DI, isolated glucocorticoid
CC deficiency, hyperfunctioning thyroid adenomas, familial hypocalciuric
CC hypercalcaemia, hyperparathyroidism and neurological disorders. The
CC methods may be used for screening pluralities of test compounds (e.g. a
CC small molecule library of compounds) or a composition containing a
CC plurality of GPCRs. The methods may be used in screening assays for
CC identification of natural and surrogate agonists of orphan GPCRs, and for
CC identification of GPCR antagonists and/or agonists
XX
XX Sequence 418 AA;

Query Match	45.5%;	Score 897.5;	DB 4;	Length 418;
Best Local Similarity	46.8%;	Pred. No. 1.8e-84;		
Matches 178; Conservative	76;	Mismatches 113;	Indels 13;	Gaps 5;

Qy	6	KVFKKCAPNGKVTLYMGRDVFVDHVSVEPIDGIVLDDDEYIRDNRKVFGQIVCSFRYGR	65
Db	7	RVFKKASPNGLTVYLGRDFVDHIDLVDVPDGVVLVDPEYLKE-RRVVVTLTCAFRYGR	65
Qy	66	EEDVWMLNFOKEICLASEQIYPRPEKSDEQTKLOERLLKGGSNAIPFTENISPNAPS	125
Db	66	EDLDVLGLTRFKDLFVANVQSFPAPBEDKKPLTRLQERLIKKGEHAYPETFEIPNLPC	125
Qy	126	SVTLQGEGEDNDGPCSVSYVKIIFAGESETDRTHRSTVTLGIRKIOPAPTQGOQPCTL	185
Db	126	SVTLQGPEDTGKAGCVDYEVAKAFCAENLBEEKIHKNSVRLVIRKVQVAPERPGPQTAE	185
Qy	186	VKRDEMLSPEGLELEVLTLDKQLYLHGERICVNICIRNNSNKMWKIKAMVQQGVVDVVLFQ	245
Db	186	TTRQGLMSDKPLHLSEASLDKEIYYHGERPISVNVHNTNNNTKTVMKIKISVRQYADICLFN	245
Qy	246	NGSVRNTVASLETSECCPIQPGSSLQKVMVLTPLBSNNKQRGIALDGQIKRODOCLAST	305
Db	246	TAQYKCVPAMEEADD--TVAPSSSTFCCKVYTLTPFLANNREKRGALDGKLKHBDTNLASS	303
Qy	306	TLLAOPDQDAFGVATISYAVKVLF--LGALGGELSA----ELPFVLMHPKPGETK---A	355
Db	304	TLLREGANREITLGITVISYKVKVKLVESRGGLGLDLASSDVAVELPFTLMHPKPKEEPPHR	363
Qy	356	KVIHADSOADVETFERODTID	375
Db	364	EVRENETPVDTNLIELDTND	383

RESULT 14	
ID	ABG13574 standard; protein, 369 AA.
AC	ABG13574;
DT	18-FEB-2002 (first entry)
DE	Novel human diagnostic protein #13565.
KW	Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX	food supplement; medical imaging; diagnostic; genetic disorder.
OS	Homo sapiens.
PN	W0200175067-A2.
PD	11-OCT-2001.
PF	30-MAR-2001; 2001WO-US008631.
PR	31-MAR-2000; 2000US-00540217.
XX	23-AUG-2000; 2000US-00649167.
PA	(HYSE-) HYSEQ INC.
PI	Drmanac RT, Liu C, Tang YT;
DR	WPI, 2001-639362/73.
DR	N-PSDB; AAS77761.
PT	New isolated polynucleotide and encoded polypeptides, useful in
PT	diagnostics, forensics, gene mapping, identification of mutations
PT	responsible for genetic disorders or other traits and to assess
PT	biodiversity.
PS	Claim 20; SEQ ID NO 43933; 103bp; English.
XX	
XX	The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX	sequences. (I) is useful as hybridisation probes, polymerase chain
XX	reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
XX	and in recombinant production of (II). The polynucleotides are also used
XX	in diagnostics as expressed sequence tags for identifying expressed
XX	genes. (I) is useful in gene therapy techniques to restore normal

QY	6	KVFKKCAPNGKVTLYMGRDFTVDHVSVEPIIDIVVLDEYIRDNKRYFGQIVCSFRYGR	65
Db	7	RVEFKASPNKGLTVYLGKRFVDHIDILVDVPDGVVLDPYELKE--RRVYVTLTCAFRYGR	65
QY	66	BEDEVMLNFOKELCLASFOIYPRPEKSDKEQTKLOERLLKKGLSNAIPFTNISPNAPS	125
Db	66	EDLDVLTGLTFERKDLFVANVQSFPPAPEDKKPLTRLOERLIKGLGEHAYFTTEIPNLPC	125
QY	126	SVTLQOGEDDNDGPPCGSVYYVKIFAGESETDRTHRRSTVTLGIRKIQFAPTKQGOQPC	125
Db	126	SVTLQGPBEDTGTACGVDEAKAFCAENLEEKIKHRNSVGLVIRKQYAPERPQPTAE	185
QY	186	VRKDFMLSPGELFVTLDKOYLHGERIGVNICIRNNSNKKVKKIRAMVQGVVDVLFQ	185
Db	186	TTRQFLMSDKPLHLFASLDKEIYYHGEPISVNVHVTNNNTKVTXIKIRISVQYADICL	245
QY	246	NGSYRNTVASLETSEGCPIPEGSSLOKVWYLTPLSSNKKORGIALLDGOIKRODQCLAST	245
Db	246	TAQYKCPVAMEEADD--TWAPSTFCRYTTLTFLANNREKGLALDGLKHEDTNLASS	305
QY	306	TLLAQPDDORDAFGVIIISYAVKVLFLGALGELTSABLPFVLMHPK--GYTA	303
Db	304	TLLREGANREIILGIVSYKVKVLV--SRGGDAVELPFTLMHPKAQRGTPA	354

RESULT	15
AAG67785	
ID	AAG67785 standard; protein; 382 AA.
XX	
AC	AAG67785;
XX	
DT	10-DEC-2001 (first entry)
XX	
DE	An exemplary phosphorylation-independent arrestin mutant.
XX	
KW	Arrestin; phosphorylation-independent arrestin mutant.
KW	G protein-coupled receptor; GPCR; GPCR ligand; retinitis pigmentosa;
KW	stationary night blindness; colour blindness; nephrogenic Di;
KW	isolated glucocorticoid deficiency; hyperfunctioning thyroid adenoma;
KW	familial hypocalcaemic hypercalcaemia; hyperparathyroidism;
KW	neurological disorder.
XX	
OS	Unidentified.
XX	
PN	WO200167106-A2.
XX	
PD	13-SEP-2001.
XX	
Pf	05-MAR-2001; 2001WO-US007304.
XX	
PR	03-MAR-2000; 2000US-0186706P.

CC The present sequence represents an exemplary phosphorylation-independent
 CC arrestin mutant. Such mutants are used in screening assays to identify
 CC ligands and/or modulators of G protein-coupled receptors (GPCRs). A
 CC method for identifying a GPCR ligand comprises contacting a composition
 CC comprising the GPCR and a constitutively active arrestin mutant with a
 CC test compound; and determining the ability of the test compound to
 CC modulate binding of arrestin mutant to the GPCR, where modulation of
 CC binding indicates that the test compound is a GPCR ligand. The method is
 CC used for identifying potential ligands and/or modulators of GPCRs,
 CC particularly modulators, for use as human therapeutics. Modulators of
 CC GPCR may be used for treating patients having e.g. retinitis pigmentosa,
 CC stationary night blindness, colour blindness, neoprogenic DI, isolated
 CC glucocorticoid deficiency, hyperfunctioning thyroid adenomas, familial
 CC hypocalcaemic hypercalcaemia, hyperparathyroidism and neurological
 CC disorders. The methods may be used for screening pluralities of test
 CC compounds (e.g. a small molecule library of compounds) or a composition
 CC containing a plurality of GPCRs. The methods may be used in screening
 CC assays for identification of natural and surrogate agonists of orphan
 CC GPCRs, and for identification of GPCR antagonists and/or agonists
 XX
 SQ Sequence 382 AA;

Query Match	44.9%;	Score 885;	DB 4;	Length 382;
Best Local Similarity	48.3%;	Pred. No. 3.1e-83;		
Matches 167;	Conservative 77;	Mismatches 98;	Indels 4;	Gaps 3;
QY	6	KVFKKCAPNGKVTLYMGRKDFVDHVSGEPIEDGLVLLDDEYIRDNRRKVFQGIYCSFRYGR	65	
Db	8	RVFKKSSPNCKLTIVYLIGKRDFFVDHDKVDPVGDVVLVDVDYIKD-RKVFVTLTCAFRYGR	66	
QY	66	EEDFVGMLNQKELCLASEQIYPPPEKSDKEQTKLOERLLKKGSAIIPFTENISNPAPS	125	
Db	67	EDLDVLGLSFRKDLFIATYQAFPPVPNPPRPPTRLQRLRLKGLQAHFFFTIIPQNLPC	126	
QY	126	SVTLQOGEEDNDGDPGCVSYVYKIFAGESEFDRTHRSTVTLGIRKIQFAPTKQGOQPTL	185	
Db	127	SVTLQPPPEDTGKACGVDFEIRAFCAKSLBEKSHKQNSVRLAIRKVQFAPEKPGQPSAE	186	
QY	186	VRKDFMLSPGELEVLTDKQLYLHGERIGVNICIRNNSNKVKKIKAMVQOGVDVTLFQ	245	
Db	187	TTTRHFLMSDRSLHLFEASLDKELYYHGEPLNVNVAHTNNSTKTVKKIKSVROYADICLFS	246	
QY	246	NGSFRNTVASIETSEGCPIQPGSSLOKVMYLTPLLSNKRORGIALDQIKRQDOCLAST	305	
Db	247	TAQYKCPVAQLEQDD--QVSPSSFTFCVKVYITTPLLSDNREKRGALDGLKHEDTNLASS	304	
QY	306	TLLAQPDQDAFGVITISYAVKVKLFLGALGELSALBPFVLMHPK	351	
Db	305	TIVKEGANKEVILGIVLSYRVKVKLVV-SRGGDVSVLELPFVLMHPK	349	

Search completed: February 9, 2005, 23:42:08
Job time : 167 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 9, 2005, 23:44:27 ; Search time 43 seconds
(without alignments)
664.897 Million cell updates/sec

Title: US-10-056-405-2

Perfect score: 1973
Sequence: 1 MYYNFKVFKKCAPNGKVTLY.....ADVETFRQDTIDQASVDFE 383

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/1/iaa/PCtUS_COMB.pep:*
- 6: /cgn2_6/ptodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	907.5	46.0	410	4	US-09-880-137-3 Sequence 3, Appli
2	903.5	45.8	418	4	US-09-880-137-1 Sequence 1, Appli
3	897.5	45.5	418	4	US-09-880-137-2 Sequence 2, Appli
4	885	44.9	382	4	US-09-880-137-8 Sequence 8, Appli
5	885	44.9	409	4	US-09-880-137-4 Sequence 4, Appli
6	880	44.6	409	4	US-09-880-137-7 Sequence 7, Appli
7	853.5	43.3	401	4	US-09-949-016-8383 Sequence 8383, Ap
8	853.5	43.3	401	4	US-09-949-016-8384 Sequence 8384, Ap
9	780.5	39.6	388	4	US-09-880-137-6 Sequence 6, Appli
10	779.5	39.5	388	4	US-09-880-137-5 Sequence 5, Appli
11	767.5	38.9	315	4	US-09-949-016-9940 Sequence 9940, Ap
12	316	16.0	197	4	US-09-270-767-58832 Sequence 58832, A
13	316	16.0	475	4	US-09-270-767-43475 Sequence 43475, A
14	225	11.4	137	4	US-09-270-767-32381 Sequence 32381, A
15	225	11.4	137	4	US-09-270-767-47598 Sequence 47598, A
16	101	5.1	363	4	US-09-270-767-44161 Sequence 44161, A
17	99.5	5.0	600	4	US-09-569-037-4 Sequence 4, Appli
18	95.5	4.8	1034	4	US-09-543-681A-8172 Sequence 8172, Ap
19	92.5	4.7	1651	1	US-08-447-411-2 Sequence 2, Appli
20	91.5	4.6	416	3	US-09-007-476-2 Sequence 2, Appli
21	91	4.6	866	4	US-09-134-000C-4363 Sequence 10219, A
22	89.5	4.5	539	4	US-09-134-000C-4363 Sequence 4363, Ap
23	89.5	4.5	725	3	US-08-425-843-2 Sequence 2, Appli
24	88	4.5	1729	4	US-09-553-690-2 Sequence 2, Appli
25	86.5	4.4	684	4	US-09-636-215-775 Sequence 775, App
26	86.5	4.4	684	4	US-09-685-166A-775 Sequence 775, App
27	86.5	4.4	684	4	US-09-679-426-775 Sequence 775, App

28	86.5	4.4	684	4	US-09-759-143-775 Sequence 775, App
29	86.5	4.4	684	4	US-09-651-236-775 Sequence 775, App
30	86.5	4.4	1030	3	US-09-091-117-2 Sequence 2, Appli
31	86	4.4	657	4	US-09-248-796A-19232 Sequence 19232, A
32	86	4.4	714	3	US-09-422-869-22 Sequence 22, Appli
33	86	4.4	714	4	US-09-538-092-867 Sequence 867, App
34	85.5	4.3	800	4	US-09-583-110-2916 Sequence 2916, Ap
35	85.5	4.3	801	4	US-09-107-433-4536 Sequence 4536, Ap
36	85	4.3	477	4	US-09-270-767-43701 Sequence 43701, A
37	85	4.3	783	1	US-08-843-521-2 Sequence 2, Appli
38	85	4.3	783	3	US-09-012-871-2 Sequence 2, Appli
39	85	4.3	1137	4	US-09-252-991A-24829 Sequence 24829, A
40	84.5	4.3	415	3	US-09-134-001C-4817 Sequence 4817, Ap
41	84.5	4.3	493	4	US-09-543-681A-7520 Sequence 7520, Ap
42	84.5	4.3	511	4	US-09-489-039A-14257 Sequence 14257, A
43	84.5	4.3	943	4	US-09-902-540-10641 Sequence 10641, A
44	84	4.3	626	4	US-09-248-796A-14855 Sequence 14855, A
45	84	4.3	1702	3	US-08-296-791-5 Sequence 5, Appli

ALIGNMENTS

RESULT 1									
US-09-880-137-3									
Sequence 3, Application US/09880137									
Patent No. 6640025									
GENERAL INFORMATION:									
APPLICANT: Berstein, Gabriel									
TITLE OF INVENTION: METHODS OF ASSAYING FOR G									
FILE REFERENCE: MNI-131									
CURRENT APPLICATION NUMBER: US/09/880,137									
CURRENT FILING DATE: 2001-03-05									
PRIOR APPLICATION NUMBER: US 60/186,706									
PRIOR FILING DATE: 2000-03-03									
NUMBER OF SEQ ID NOS: 8									
SOFTWARE: FastSeq for Windows Version 4.0									
SEQ ID NO 3									
LENGTH: 410									
TYPE: PRT									
ORGANISM: Homo sapiens									
US-09-880-137-3									
Query Match									
Best Local Similarity 46.0%; Score 907.5; DB 4; Length 410;									
Matches 176; Conservative 78; Mismatches 112; Indels 7; Gaps 4;									
Qy	6	KVFKKCAPNGKVTLYNGKRDVHDVSGVEPIDGIYVLDDEYIRDNRKVFQIVCSFRYGR	65						
Db	7	RVFKKASPNGLTVYLGKRDVHDIDLVDVGDVVLVDEYLKE-RRVYVTLTCAFRYGR	65						
Qy	66	EEDVNGLNFQKELCLASEQIYPRPEKSDKEQTKLOERLLKLGSMNIPFTFNISPNAS	125						
Db	66	EDLDVGLTFRKDLFVANVQSPFPADEKPLTRLOERLLKLGEMHYPFTFEIPNLD	125						
Qy	126	SVTLQGEDDNGDPCGVSYVVKIFAGESETDRTHRSVTTLGIRKIQFAPTKGQOQPTL	185						
Db	126	SVTLQGPEDTGKACGVDEVKAFCAENLEKIHKNSVRLVIRKQYAPERPQPPTAE	185						
Qy	186	VRKDFMLSPGELEVTLDKQLYLHGERIGVNICIRNNSNMVKIKAMVQGVVLFQ	245						
Db	186	TTRQFLMSDKPLHLLEASLDKEIYHGPISVNVHVTNNTKTIVKIKISVRQYADICLFN	245						
Qy	246	NGSYRNTVASLETSEGPQPGSSLOKVMYLLPPLSSNKORGIALDQIKRODCLAST	305						
Db	246	TAQYKCPVAMEEADD--TVAPSSTFCKVYTLTPFLANNREKRGALDGKLKHEDTNLASS	303						
Qy	306	TLLAPDORDAFGVITISYAVKVLFLGALGGELSAELPFLMHKPGTK--AKVJHADS	362						
Db	304	TLLREGANREILGIIVSYKVKVL-VESRGGDAVAELPFTLMHPKKEPPHREVENET	362						
Qy	363	QADVETFRQDTID 375							

Db 363 PVDNLIELDTND 375

```
RESULT 2
US-09-880-137-1
; Sequence 1, Application US/09880137
; Patent No. 6640025
; GENERAL INFORMATION:
; APPLICANT: Berstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; FILE REFERENCE: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
; CURRENT APPLICATION NUMBER: US/09/880,137
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186,706
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-880-137-1
```

Query Match
Best Local Similarity 45.8%; Score 903.5; DB 4; Length 418;
Matches 179; Conservative 76; Mismatches 112; Indels 13; Gaps 5;

```
QY 6 KVFKKCAPNGKVTLYMGKDFVDHVSVEPIDGIVLDDIYIRDNKRVFGQIVCSFRYGR 65
DB 7 RVFKKASPNKLTIVYLGKDFVDHIDLVEPVGVLDPEYLKE-RRVYVTLTCAFRYGR 65
QY 66 EEDVWGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKLGSNAPFTFNISPNAPS 65
DB 66 EDLDVLGLTRKDLFVANVQSPFPAPEDKKPLTRLQERLLKLGSHAYPFTFEIPNLP 125
QY 126 SVTLQGGEDNDGDCGVSYYVKIFAGESEDTDRHRSVTTLGIRKIQFAPTKOQOQPC 125
DB 126 SVTLQGGEDNDGDCGVSYYVKIFAGESEDTDRHRSVTTLGIRKIQFAPTKOQOQPC 185
QY 126 SVTLQGGEDNDGDCGVSYYVKIFAGESEDTDRHRSVTTLGIRKIQFAPTKOQOQPC 185
DB 126 SVTLQGGEDNDGDCGVSYYVKIFAGESEDTDRHRSVTTLGIRKIQFAPTKOQOQPC 185
QY 186 VRKDFMLSPGELLEVTLDKQLYLHGERIGVNICIRNSNKKWKIKAMVQGVVDFQ 245
DB 186 TTRQFLMSDKPLHLASLDKEIYHGEPISVNVHTNNTKTVKKIKISVQYADICLEN 245
QY 246 NGSYRNTVASLETSEGCPIQPGSSLOKVMYLTPLSSNKQRGIALDQIKRODOCLAST 245
DB 246 TAQYKCPVAMEEADD--TVAPSSSTFCVKYTLTPFLANNREKGLALDGKLKHEDTNLASS 303
QY 306 TLLAOPDQDAFGVITISYAVKVLFL--GALGELSA-----ELPFVLMHPKPGTK--A 355
DB 304 TLLREGANREILGITIVSYKVKVLVSRGGLGLDASSDVAVELPFTLMHPKPEEPHR 363
QY 356 KVIHADSQADVETFRQDTID 375
DB 364 EVPEHETPVDNLIELDTND 383
```

```
RESULT 3
US-09-880-137-2
; Sequence 2, Application US/09880137
; Patent No. 6640025
; GENERAL INFORMATION:
; APPLICANT: Berstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; FILE REFERENCE: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
; CURRENT APPLICATION NUMBER: US/09/880,137
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186,706
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 2
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-137-2
```

Query Match
Best Local Similarity 45.5%; Score 897.5; DB 4; Length 418;
Matches 178; Conservative 76; Mismatches 113; Indels 13; Gaps 5;

```
QY 6 KVFKKCAPNGKVTLYMGKDFVDHVSVEPIDGIVLDDIYIRDNKRVFGQIVCSFRYGR 65
DB 7 RVFKKASPNKLTIVYLGKDFVDHIDLVEPVGVLDPEYLKE-RRVYVTLTCAFRYGR 65
QY 66 EEDVWGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKLGSNAPFTFNISPNAPS 65
DB 66 EDLDVLGLTRKDLFVANVQSPFPAPEDKKPLTRLQERLLKLGSHAYPFTFEIPNLP 125
QY 126 SVTLQGGEDNDGDCGVSYYVKIFAGESEDTDRHRSVTTLGIRKIQFAPTKOQOQPC 125
DB 126 SVTLQGGEDNDGDCGVSYYVKIFAGESEDTDRHRSVTTLGIRKIQFAPTKOQOQPC 185
QY 186 VRKDFMLSPGELLEVTLDKQLYLHGERIGVNICIRNSNKKWKIKAMVQGVVDFQ 245
DB 186 TTRQFLMSDKPLHLASLDKEIYHGEPISVNVHTNNTKTVKKIKISVQYADICLEN 245
QY 246 NGSYRNTVASLETSEGCPIQPGSSLOKVMYLTPLSSNKQRGIALDQIKRODOCLAST 245
DB 246 TAQYKCPVAMEEADD--TVAPSSSTFCVKYTLTPFLANNREKGLALDGKLKHEDTNLASS 303
QY 306 TLLAOPDQDAFGVITISYAVKVLFL--GALGELSA-----ELPFVLMHPKPGTK--A 355
DB 304 TLLREGANREILGITIVSYKVKVLVSRGGLGLDASSDVAVELPFTLMHPKPEEPHR 363
QY 356 KVIHADSQADVETFRQDTID 375
DB 364 EVPEHETPVDNLIELDTND 383
```

```
RESULT 4
US-09-880-137-8
; Sequence 8, Application US/09880137
; Patent No. 6640025
; GENERAL INFORMATION:
; APPLICANT: Berstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; FILE REFERENCE: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
; CURRENT APPLICATION NUMBER: US/09/880,137
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186,706
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Homo sapiens mutation
US-09-880-137-8
```

Query Match
Best Local Similarity 44.9%; Score 885; DB 4; Length 382;
Matches 167; Conservative 77; Mismatches 98; Indels 4; Gaps 3;

```
QY 6 KVFKKCAPNGKVTLYMGKDFVDHVSVEPIDGIVLDDIYIRDNKRVFGQIVCSFRYGR 65
DB 8 RVFKKASPNKLTIVYLGKDFVDHIDLVEPVGVLDPEYLKE-RRVYVTLTCAFRYGR 66
QY 66 EEDVWGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKLGSNAPFTFNISPNAPS 125
DB 67 EDLDVLGLSPKDLFLATYQAFPPVNPBPPTRLQDRLLKLGQAHHEFFFTIPQNLPC 126
```

```

QY      126 SVTLQGGEDDNGDPCCGVSYVYKIFAGESETDRTHRSTRVTLGIRKIQEPATKQGOQPCPTL 185
      |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      127 SVTLQGPPEDTGKACGVDFEIRAFCAKSLIEEKSHKRNSVRLVIRKVFAPAEKPGPQPSAE 186
QY      186 VRKDEMLSPGELLEVTLDKQLYLHGERLGVNICIRNNSNMKVKKIKAMVQGVDPVLFQ 245
      ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      187 TTRHFLMSDRSLHLEASLDKELYYHGEPLNVNVHTNNSRTKTVKKIKVSRQYADICLFS 246
QY      246 NGSYRNTVASLETSEGCPIQPGSSLQKVMYLTPLLSNKRGRGIALDGIKRDQCLAST 305
      ::|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      247 TAQYKCPVAQLEQDD--QVSPSSTFCXVYTTPLLSDBNEKRGLALDGKLGHEDTNLAAS 304
QY      306 TLLAQPDQDAFGVIISYAVKVKLFLGALGGELSAELPFLMHKPK 351
      ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      305 TIIVEGANKEVLLGILVSTRVKVKLVV--SRGGDVSVELPFLMHKPK 349

```

```

RESULT 5
US-09-880-137-4
; Sequence 4, Application US/09880137
; Patent No. 6640025
; GENERAL INFORMATION:
; APPLICANT: Barstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
; FILE REFERENCE: MNI-131
; CURRENT APPLICATION NUMBER: US/09/880,137
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186,706
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 4
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-137-4

```

Query Match	44.9%;	Score 885;	DB 4;	Length 409;
Best Local Similarity	48.3%;	Pred. No. 6.6e-85;		
Matches 167;	Conservative 77;	Mismatches 98;	Indels 4;	Gaps 3;

[illegible]

RESULT 6
US-09-880-137-7
; Sequence No., Application US/09880137
; Patent No. 6640025
; GENERAL INFORMATION:

```

? APPLICANT: Berstein, Gabriel
? ?
? ? TITLE OF INVENTION: METHODS OF ASSAYING FOR G
? ? TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
? ? FILE REFERENCE: MNI-131
? ?
? ? CURRENT APPLICATION NUMBER: US/09/880,137
? ? CURRENT FILING DATE: 2001-03-05
? ? PRIOR APPLICATION NUMBER: US 60/186,706
? ? PRIOR FILING DATE: 2000-03-03
? ? NUMBER OF SEQ ID NOS: 8
? ? SOFTWARE: FastSeq for Windows Version 4.0
? ? SEQ ID NO 7
? ? LENGTH: 409
? ? TYPE: PRT
? ?
? ? ORGANISM: Artificial Sequence
? ?
? ? FEATURE:
? ? OTHER INFORMATION: Description of Artificial Sequence: Homo sapiens mutation
US-09-880-137-7

```

Query Match	44.6%;	Score 880;	DB 4;	Length 409;
Best Local Similarity	48.0%;	Pred. No. 2.2e-84;		
Matches 166;	Conservative 77;	Mismatches 99;	Indels 4;	Gaps 3;

```

QY      6 KYFKKCAPNGKVTLLYMGKRDVFDVHVSVEPIDGIVLNDEYIRDNKRVFGQIVCSFRYGR  65
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      8 RVEFKSSPNCKLTVYLGKRDVFDHLDKVDVVDGVVLVDPDYLKD-RKVFTVLTCAFRYGR  66

QY      66 EEDVEWGLNFQKELCLASEQIYPRPEKSDEKQTKQERLLKKLGSAIIPFTENISPAWS  125
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      67 EDLDVLGLSFRKDLFIATYQAFPPVYENPPRPPTRLQDRLLRKLGGQAHPPFFTIPQNIIPC  126

QY      126 SVTLQOGEDNDGPPCGVSYYVKIFAGESETDRTHRSTVTLGIRKIQFAPTKOGQOQPECTL  185
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      127 SVTLQPGPEDTGRACGVDFEIRAFCAKSLSEKSHKNSVRLVIEKQFAPEKGPQPSAB  186

QY      186 VRKDFMLSPGELSEVTLDKQLYHGERIGVNICIRNNSNMKVKIKIAMVQOGVDVVLFEQ  245
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      187 TTHHFLMSDRSLHLEASLDKELYHGEPLNVNVHTNNSTKTVKIKIVSVRQYADICHS  246

QY      246 NGSYRNTVASLETSEGCPIQPGSSLOQVMYLTPLSSNNKQRGIALDGOIKRQDQCLAST  305
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      247 TAYQKCPVAQLEQDD--QVSPSSTFCVKYTTITPLSDNREKRGALDGKXKHEDTNLASS  304

QY      306 TLLAQPDDQRDAFGVIISYAVKVKLFLGALGSELSAELPFVLMHPKP  351
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      305 TIYKEGANKEVGLIVSYRVKVKLVV-SRGGDVSVLELPFVLMHPKP  349

```

RESULT 7
US-09-949-016-8383
; Sequence 8383, Application US/09949016
; Patent No. 6812339

```

? APPLICANT: VENTER, J. Craig et al.
? TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
? TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
? FILE REFERENCE: CL001307
? CURRENT APPLICATION NUMBER: US/09/949,016
? CURRENT FILING DATE: 2000-04-14
? PRIOR APPLICATION NUMBER: 60/241,755
? PRIOR FILING DATE: 2000-10-20
? PRIOR APPLICATION NUMBER: 60/237,768
? PRIOR FILING DATE: 2000-10-03
? PRIOR APPLICATION NUMBER: 60/231,498
? PRIOR FILING DATE: 2000-09-08
? NUMBER OF SEQ ID NOS: 207012
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 8383

```

TYPE: PRT
ORGANISM: Human
US-09-949-016-8383

Query Match 43.3%; Score 853.5; DB 4; Length 401;

Best Local Similarity 46.1%; Pred. No. 1.4e-81;
Matches 170; Conservative 75; Mismatches 111; Indels 13; Gaps 5;

```
QY 17 VTLVWGKRDVFDVHVSVEPIDGIVLDDDEYIRDNKRVFGQIVCSFRYGRDEDEVMGLNFQ 76
Db 1 LTVYLGKRDVFDHIDLVDVPGVVLVDPEYLKE-RRVYVTLTCAFRYGREDDLDVLGLTFR 59
QY 77 KELCLASEQIYPRPEKSDKEQTKLQERLLKLGSNAPFTFNISPNAPSSVTLLQOGEDDN 136
Db 60 KDLFVANVQSFPPAPEDKKPLTRLQERLLKLGEGHAYPFTEIPNLPSCSVTLQGPEDT 119
QY 137 GPCGVSYVVKIFAGESETDTRHRSSTVTLGIRKIQFAPTKOGQOPCTLVKDFMLSPGE 196
Db 120 GKACGVDEYVKAFCANLEEKIKHKNVRLVIRKQYAPERPQPTAETTRQFLMSDKP 179
QY 197 LELEVTLDKQLYLHGERIGVNICIRNNSNKMVKIKAMVQGVVLFQNGSYRNTVASL 256
Db 180 LHLEASLDKEIYYHGEPISVNVHVTNTNTKTKIKISVQYADICLFNTAQYKCPVAME 239
QY 257 ETSEGCPIQPGSSLOKWMTLPLSSNKGRIALDGOIKRQDQCLASTTLIAQPDQDA 316
Db 240 EADD--TVAPSTFCKVYTLTLPFANNREKRGALDGLKHEDTNLASSTLREGANREI 297
QY 317 FGVII SYAVKVKFL--GALGELSA-----ELPFVLMHPKPGTK--AKVIHADSOADV 366
Db 298 LGIIVSYKVKVKLVSRRGLLDGLASSDVAVELPFTLMHPKPEEPHREVPENETPVDT 357
QY 367 ETRQDTID 375
Db 358 NLIELDTND 366
```

RESULT 8
US-09-949-016-8384

```
/ Sequence 8384, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ FILE REFERENCE: C1001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ PRIOR FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 8384
/ LENGTH: 401
/ TYPE: PRT
/ ORGANISM: Human
US-09-949-016-8384
```

Query Match
Best local Similarity 46.1%; Score 853.5; DB 4; Length 401;
Matches 170; Conservative 75; Mismatches 111; Indels 13; Gaps 5;

```
QY 17 VTLVWGKRDVFDVHVSVEPIDGIVLDDDEYIRDNKRVFGQIVCSFRYGRDEDEVMGLNFQ 76
Db 1 LTVYLGKRDVFDHIDLVDVPGVVLVDPEYLKE-RRVYVTLTCAFRYGREDDLDVLGLTFR 59
QY 77 KELCLASEQIYPRPEKSDKEQTKLQERLLKLGSNAPFTFNISPNAPSSVTLLQOGEDDN 136
Db 60 KDLFVANVQSFPPAPEDKKPLTRLQERLLKLGEGHAYPFTEIPNLPSCSVTLQGPEDT 119
QY 137 GPCGVSYVVKIFAGESETDTRHRSSTVTLGIRKIQFAPTKOGQOPCTLVKDFMLSPGE 196
Db 120 GKACGVDEYVKAFCANLEEKIKHKNVRLVIRKQYAPERPQPTAETTRQFLMSDKP 179
```

```
QY 197 LELEVTLDKQLYLHGERIGVNICIRNNSNKMVKIKAMVQGVVLFQNGSYRNTVASL 256
Db 180 LHLEASLDKEIYYHGEPISVNVHVTNTNTKTKIKISVQYADICLFNTAQYKCPVAME 239
QY 257 ETSEGCPIQPGSSLOKWMTLPLSSNKGRIALDGOIKRQDQCLASTTLIAQPDQDA 316
Db 240 EADD--TVAPSTFCKVYTLTLPFANNREKRGALDGLKHEDTNLASSTLREGANREI 297
QY 317 FGVII SYAVKVKFL--GALGELSA-----ELPFVLMHPKPGTK--AKVIHADSOADV 366
Db 298 LGIIVSYKVKVKLVSRRGLLDGLASSDVAVELPFTLMHPKPEEPHREVPENETPVDT 357
QY 367 ETRQDTID 375
Db 358 NLIELDTND 366
```

RESULT 9
US-09-880-137-6

```
/ Sequence 6, Application US/09880137
/ Patent No. 6640025
/ GENERAL INFORMATION:
/ APPLICANT: Berstein, Gabriel
/ TITLE OF INVENTION: METHODS OF ASSAYING FOR G
/ FILE REFERENCE: MNI-131
/ CURRENT APPLICATION NUMBER: US/09/880,137
/ CURRENT FILING DATE: 2001-03-05
/ PRIOR APPLICATION NUMBER: US 60/186,706
/ PRIOR FILING DATE: 2000-03-03
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 6
/ LENGTH: 388
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-880-137-6
```

Query Match
Best local Similarity 39.6%; Score 780.5; DB 4; Length 388;
Matches 166; Conservative 79; Mismatches 125; Indels 19; Gaps 7;

```
QY 6 KVFKKCAPNGKVTLYMGKRDVFDVHVSVEPIDGIVLDDDEYIRDNKRVFGQIVCSFRYGR 65
Db 3 KVFKKTSNGKLTLYLGRDVFHDVDTVEPIDGVVLDPPEYLK-CKLFLVMTLCARRYGR 61
QY 66 EEDFVGLNFOKELCLASEQIYPRPEKSDK-EQTKLQERLLKLGSNAPFTFNISPNAP 124
Db 62 DDLVETIGLTFRKDLVYQTLQVVPASSSPQALTVLQERLLKLGDNAYPFTLQMTNLP 121
QY 125 SSTVLLQOGEDNDPCGVSYVVKIFAGESETDTRHRSSTVTLGIRKIQFAPTKOGQOPCT 184
Db 122 CSVTLLQGPEDAGKPCGIDPEVKSFCANPEETVSKRDYVRLVVRKQFAPPEAGPGPSA 181
QY 185 LVKDFMLSPGELELEVTLDKQLYLHGERIGVNICIRNNSNKMVKIKAMVQGVVLF 244
Db 182 QTIIRFLISAQPLQLQAMMDREVHYHGEPISVNVSIINNTNKVIKIKISVDQITDVLY 241
QY 245 QNGSYRNTVASLETSEGCPIQPGSSLOKWMTLPLSSNKGRIALDGOIKRQDCLAS 304
Db 242 SLDKYTKVFIQEFTE--TVANSSFSQSFAPVTPILAAASCQKRGALDGLKHEDTNLAS 299
QY 305 TTLAQPQDQDAFGVII SYAVKVKFL--GALGELSA-----ELPFVLMHPKPGTKAKV 357
Db 300 STIIRGMDKELLGILVSYKVVNLMWSCGILGLDGLTASDVVELPLVLIHPKPSHAA- 358
QY 358 IHADSOADV--ETFRQDTIDQASVDFE 383
Db 359 -----SSEDIIVIEFTTRKGEESQKAVEAE 383
```

RESULT 10
US-09-880-137-5

```

; Sequence 5, Application US/09880137
; Patent No. 6640025
; GENERAL INFORMATION:
; APPLICANT: Berstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
; FILE REFERENCE: MNI-131
; CURRENT APPLICATION NUMBER: US/09/880,137
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186,706
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-137-5

```

Query Match	39.5%;	Score 779.5;	DB 4;	Length 388;
Best Local Similarity	42.4%;	Pred. No. 9.3e-74;		
Matched 165;	Conservative 80;	Mismatches 125;	Indels 19;	Gaps 7;

[illegible]

```

RESULT 11
US-09-949-016-9940
; Sequence 9940, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9940
;
; LENGTH: 315

```

```

; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9940

```

Query Match	38.9%;	Score 767.5;	DB 4;	Length 315;
Best Local Similarity	48.0%;	Pred. No. 1.12e-72;		
Matches 145;	Conservative 66;	Mismatches 88;	Indels 3;	Gaps 2;

QY	6	KVEKKCAPNGKVTLYMGKRD	FVDHVS	GVEPIDIGI	VLLDDEYIRDN	KVFGOI	VCSFR	YGR	65
		: : : :	: : : :	: : : :	: : : :	: : : :	: : : :	: : : :	
Db	8	RVEKKSSPNCKLTVYLGKRD	FVDHLDKVD	PVDGVVLD	PDYIKD	-RKVFVTL	TCAFR	YGR	66
QY	66	EEDFWMGLNFQKELCLASE	OIYPRE	BKSDKEQ	TKQERLLK	LGSNAIP	FTFNIS	PNAPS	125
		: : : :	: : : :	: : : :	: : : :	: : : :	: : : :	: : : :	
Db	67	EDLDVLGLSFRKDLFIAT	YQAFPR	VYVNP	PRPPTRL	QDRLLRKL	GQHAP	FEFTIPQ	126
QY	126	SVTLQOGEDDNGDEPCVS	YVYKIPAGE	SETDRTHR	STVTLGIR	KIOFAPT	KOGQOP	CTL	185
		: : : :	: : : :	: : : :	: : : :	: : : :	: : : :	: : : :	
Db	127	SVTLQGPEDTCKACGV	DFEIRAF	CAKSL	EKSHKNS	SVRLVIR	KVQFA	EKPGPQ	186
QY	186	VRKDFMLSPGELE	VTLLDKQ	LYLHGER	IGVNICIR	NNSNKM	VKKIKAM	VYQGV	245
		: : : :	: : : :	: : : :	: : : :	: : : :	: : : :	: : : :	
Db	187	TTHHFLMSDRSLH	EASLDKEL	YHGEPL	NVNVHT	TNNSTKT	VYKIKIV	SVRQY	246
QY	246	NGSVRNTVASLET	SEGCPIQ	PGSSLO	KVMYLT	PLSSNK	QRGIAL	DCQIKR	305
		: : : :	: : : :	: : : :	: : : :	: : : :	: : : :	: : : :	
Db	247	TAQYKCPVAQLE	QDD--Q	VSPSSIT	FCVVYTT	ITPL	SSDNRE	KRGIAL	304
QY	306	TL	307						
		: :							
Db	305	TM	306						

```

RESULT 12
US-09-270-767-58832
; Sequence 58832, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58832
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-58832

```

```

Query Match          16.0%; Score 316; DB 4; Length 197;
Best Local Similarity 49.6%; Pred. No. 4.3e-25;
Matches 59; Conservative 25; Mismatches 33; Indels 2; Gaps 1;

Qy      235 VQGVDVVLFGNGSYRNTVASLETSEGCPIOPGSSLQKVMYLTPLSSNKKORGIALDQ 294
        |||:|||||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db       2 VRQFADICLFSTAQYKSVVAEIESEDGCQVAGFTLSKVPELCPLLANNKDWGLALDQ 61

Qy      295 IKRQDCLASTLLAOPDDDAFGVIISYAVNKVKLFLGA--LGELSAELEPVLMPKP 351
        ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db       62 LKHEDTNLASSTLITNPACRESLGIMWHYKVKVLLISSPLLNGDLVAELPFLLMHPK 120

RESULT 13
US-09-270-767-43475
; Sequence 43475, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767

```

; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 43475
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
; US-09-270-767-43475

Query Match
Best Local Similarity 16.0%; Score 316; DB 4; Length 475;
Matches 59; Conservative 25; Mismatches 33; Indels 2; Gaps 1;

QY 235 VQGVVDFVLFQNGSYRNTVAVSLETSEGCPIQPGSSLOKVMYLPPLSSNKGRRGIALDQ 294
DB 280 VRQFADICLFSTAQYKSVVAEISEDCQVAFGFTLSKVFEELCPPLANNKDKWGLADQ 339
QY 295 IKRQDOCLASTTLIAQPPORDAFGVLIISYAVKVLFLGA--LGELSAELPFVLMHPKP 351
DB 340 LKHEDTNLASSTLITNPAQRESLGIWVHKVKVLLISSPLNGDLVAELPFTLMHPKP 398

RESULT 14
US-09-270-767-32381
; Sequence 32381, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 32381
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; US-09-270-767-32381

Query Match
Best Local Similarity 11.4%; Score 225; DB 4; Length 137;
Matches 52; Conservative 26; Mismatches 38; Indels 6; Gaps 4;

QY 6 KVFKKCAPNGKVTLYMGRDVFVDHVGVEP--IDGIIVLDDEYIRDNKRVFGQIVCSFRY 63
DB 19 RYVKKTSPNCVLTLYLPTREIT--LTGNPVSVLRGIVYVDPKAIQYR-VYAQLTLTFRY 75
QY 64 GREDEVWGLNFQKELCLASEQIYPRPEKSDKEQ-TKLOERLLKLGSNAIPTFNISPN 122
DB 76 GREDEVWGLRFCNEAIMSLHQIWPRLLEPTPELSPLQEALMKRLGDAHPFTLSLSY 135
QY 123 AP 124
DB 136 AP 137

RESULT 15
US-09-270-767-47598
; Sequence 47598, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 47598
; LENGTH: 137

; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; US-09-270-767-47598

Query Match
Best Local Similarity 11.4%; Score 225; DB 4; Length 137;
Matches 52; Conservative 26; Mismatches 38; Indels 6; Gaps 4;

QY 6 KVFKKCAPNGKVTLYMGRDVFVDHVGVEP--IDGIIVLDDEYIRDNKRVFGQIVCSFRY 63
DB 19 RYVKKTSPNCVLTLYLPTREIT--LTGNPVSVLRGIVYVDPKAIQYR-VYAQLTLTFRY 75
QY 64 GREDEVWGLNFQKELCLASEQIYPRPEKSDKEQ-TKLOERLLKLGSNAIPTFNISPN 122
DB 76 GREDEVWGLRFCNEAIMSLHQIWPRLLEPTPELSPLQEALMKRLGDAHPFTLSLSY 135
QY 123 AP 124
DB 136 AP 137

Search completed: February 9, 2005, 23:55:39
Job time : 45 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 9, 2005, 23:23:01 ; Search time 130 Seconds
(without alignments)
959.569 Million cell updates/sec

Title: US-10-056-405-2

Perfect score: 1973
Sequence: 1 MVYNFKVFKKCAPNGKVTLY.....ADVERTFRQDTIDQASVDFE 383

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1373511 seqs, 325702437 residues

Total number of hits satisfying chosen parameters: 1373511

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1973	100.0	383	14 US-10-094-240-2	Sequence 2, Appli
2	1973	100.0	383	14 US-10-056-405-2	Sequence 2, Appli
3	1023	51.8	398	14 US-10-094-240-25	Sequence 25, Appli
4	982.5	49.8	401	14 US-10-094-240-27	Sequence 27, Appli
5	907.5	46.0	410	9 US-09-880-137-3	Sequence 3, Appli
6	907.5	46.0	410	10 US-09-800-137A-3	Sequence 3, Appli
7	903.5	45.8	418	9 US-09-880-137-1	Sequence 1, Appli
8	903.5	45.8	418	10 US-09-800-137A-1	Sequence 1, Appli
9	903.5	45.8	452	14 US-10-038-010-52	Sequence 52, Appli
10	900.5	45.6	418	14 US-10-043-487-348	Sequence 348, App
11	897.5	45.5	418	9 US-09-880-137-2	Sequence 2, Appli
12	897.5	45.5	418	10 US-09-800-137A-2	Sequence 2, Appli
13	885	44.9	382	9 US-09-880-137-8	Sequence 8, Appli

14	885	44.9	382	10 US-09-800-137A-8	Sequence 8, Appli
15	885	44.9	409	9 US-09-880-137-4	Sequence 4, Appli
16	885	44.9	409	10 US-09-800-137A-4	Sequence 4, Appli
17	880	44.6	409	9 US-09-880-137-7	Sequence 7, Appli
18	880	44.6	409	10 US-09-800-137A-7	Sequence 7, Appli
19	869.5	44.1	410	14 US-10-038-010-54	Sequence 54, Appli
20	865	43.8	454	15 US-10-369-493-6702	Sequence 6702, Ap
21	780.5	39.6	388	9 US-09-880-137-6	Sequence 6, Appli
22	780.5	39.6	388	10 US-09-800-137A-6	Sequence 6, Appli
23	779.5	39.5	388	9 US-09-880-137-5	Sequence 5, Appli
24	779.5	39.5	388	10 US-09-800-137A-5	Sequence 5, Appli
25	379.5	19.2	466	16 US-10-722-357-31	Sequence 31, Appli
26	361.5	18.3	212	14 US-10-106-698-4673	Sequence 4673, Ap
27	173	8.8	65	9 US-09-864-761-45375	Sequence 45375, A
28	111	5.6	38	9 US-09-864-761-40768	Sequence 40768, A
29	98.5	5.0	349	15 US-10-335-977-5814	Sequence 5814, Ap
30	98.5	5.0	1632	16 US-10-437-963-177962	Sequence 177962,
31	95	4.8	348	15 US-10-424-599-201640	Sequence 201640,
32	94.5	4.8	1211	15 US-10-282-122A-69274	Sequence 69274, A
33	92	4.7	320	15 US-10-335-977-5813	Sequence 5813, Ap
34	92	4.7	944	15 US-10-282-122A-71708	Sequence 71708, A
35	92	4.7	1348	15 US-10-282-122A-56877	Sequence 56877, A
36	91.5	4.6	299	15 US-10-282-122A-51797	Sequence 51797, A
37	91.5	4.6	416	15 US-10-282-122A-44280	Sequence 44280, A
38	91.5	4.6	752	16 US-10-437-963-115259	Sequence 115259,
39	91.5	4.6	869	9 US-09-815-242-10623	Sequence 10623, A
40	91	4.6	498	15 US-10-369-493-2030	Sequence 2030, Ap
41	91	4.6	800	15 US-10-104-047-3534	Sequence 3534, Ap
42	90.5	4.6	492	9 US-09-881-752A-142	Sequence 142, App
43	90.5	4.6	492	15 US-10-282-122A-58846	Sequence 58846, A
44	90.5	4.6	976	16 US-10-437-963-201424	Sequence 201424,
45	90	4.6	356	14 US-10-153-398-15	Sequence 15, Appli

ALIGNMENTS

RESULT 1
US-10-094-240-2
; Sequence 2, Application US/10094240
; Publication No. US20030082637A1
; GENERAL INFORMATION:
; APPLICANT: ZWIEBEL, LAURENCE J.
; TITLE OF INVENTION: ARRESTIN GENE, POLYPEPTIDE, AND METHODS OF USE THEREOF
; FILE REFERENCE: N8289
; CURRENT APPLICATION NUMBER: US/10/094,240
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 10/056,405
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/264,649
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Anopheles gambiae
US-10-094-240-2

Query Match	Best Local Similarity	Score	DB ID	Length	Matches	Conservative	Mismatches	Indels	Gaps
1	100.0%	1973	14	383	383	0	0	0	0
QY	1	MVYNFKVFKKCAPNGKVTLYMGKRDYDVHSGVEPIDGIIVLDEYTRDNKRVFGQIVCS	60						
DB	1	MVYNFKVFKKCAPNGKVTLYMGKRDYDVHSGVEPIDGIIVLDEYTRDNKRVFGQIVCS	60						
QY	61	FRYGRBEDEVMGLNFOKELCCLASEQIYPRPEKSDKEQTKLQERLKLKLSNAIPFTNIS	120						
DB	61	FRYGRBEDEVMGLNFOKELCCLASEQIYPRPEKSDKEQTKLQERLKLKLSNAIPFTNIS	120						
QY	121	PNAPSSVTLQGGEDNGDPCGVSYVYKIFAGESETDTRHRSTVTYLGIRKIQFAPRYKQO	180						

```

Db      121  PNAASSVTLLQOGEEDNDGDCGVSYVYKIFAGESEETDRTHRESVTLTGIRKIQFAPTKQOQ 180
QY      181  QPCTLVKDFMLSPGELLEVTLTDKQLYLHGERIGVNICIRNNSNMKVKKIKAMVOQGV 240
Db      181  QPCTLVKDFMLSPGELLEVTLTDKQLYLHGERIGVNICIRNNSNMKVKKIKAMVOQGV 240
QY      241  VVLFONGSYRNTVASLETSEGCPIQPGSSLOKWMYLTPLSSNKORRGIALDGOIKRODQ 300
Db      241  VVLFONGSYRNTVASLETSEGCPIQPGSSLOKWMYLTPLSSNKORRGIALDGOIKRODQ 300
QY      301  CLASTTLLAOPDORDAFGVIIISYAVKVLFLGALGGELSAELPFVLMHPKPGTKAKAVIHA 360
Db      301  CLASTTLLAOPDORDAFGVIIISYAVKVLFLGALGGELSAELPFVLMHPKPGTKAKAVIHA 360
QY      361  DSOADVETFRQDTIDQASVDPE 383
Db      361  DSOADVETFRQDTIDQASVDPE 383

```

RESULT 2

```

; US-10-056-405-2
; Sequence 2, Application US/10056405
; Publication No. US20030166013A1
; GENERAL INFORMATION:
; APPLICANT: ZWIEBEL, LAURENCE J.
; TITLE OF INVENTION: MOSQUITO OLFACTORY GENES, POLYPEPTIDES, AND METHODS OF
; FILE REFERENCE: N7841
; CURRENT APPLICATION NUMBER: US/10/056,405
; PRIOR FILING DATE: 2002-01-24
; NUMBER OF SEQ ID NOS: 264,649
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Anopheles gambiae
US-10-056-405-2

```

Query Match

```

Best Local Similarity 100.0%; Score 1973; DB 14; Length 383;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1  MYVNFKVFKKCAPNGKVTLYMGRKDFVDHVSQVEPIDGIVLDEYIRDNKRVFGQIVCS 60
Db      1  MYVNFKVFKKCAPNGKVTLYMGRKDFVDHVSQVEPIDGIVLDEYIRDNKRVFGQIVCS 60
QY      61  FRYGREDEVMGKLFQKELCLASEQIYPRPEKSDKEQTKLQERLLKLGSAIPTFNIS 120
Db      61  FRYGREDEVMGKLFQKELCLASEQIYPRPEKSDKEQTKLQERLLKLGSAIPTFNIS 120
QY      121  PNAASSVTLLQOGEEDNDGDCGVSYVYKIFAGESEETDRTHRESVTLTGIRKIQFAPTKQOQ 180
Db      121  PNAASSVTLLQOGEEDNDGDCGVSYVYKIFAGESEETDRTHRESVTLTGIRKIQFAPTKQOQ 180
QY      181  QPCTLVKDFMLSPGELLEVTLTDKQLYLHGERIGVNICIRNNSNMKVKKIKAMVOQGV 240
Db      181  QPCTLVKDFMLSPGELLEVTLTDKQLYLHGERIGVNICIRNNSNMKVKKIKAMVOQGV 240
QY      241  VVLFONGSYRNTVASLETSEGCPIQPGSSLOKWMYLTPLSSNKORRGIALDGOIKRODQ 300
Db      241  VVLFONGSYRNTVASLETSEGCPIQPGSSLOKWMYLTPLSSNKORRGIALDGOIKRODQ 300
QY      301  CLASTTLLAOPDORDAFGVIIISYAVKVLFLGALGGELSAELPFVLMHPKPGTKAKAVIHA 360
Db      301  CLASTTLLAOPDORDAFGVIIISYAVKVLFLGALGGELSAELPFVLMHPKPGTKAKAVIHA 360
QY      361  DSOADVETFRQDTIDQASVDPE 383
Db      361  DSOADVETFRQDTIDQASVDPE 383

```

RESULT 3

```

; US-10-094-240-25
; Sequence 25, Application US/10094240
; Publication No. US20030082637A1
; GENERAL INFORMATION:
; APPLICANT: ZWIEBEL, LAURENCE J.
; TITLE OF INVENTION: ARRESTIN GENE, POLYPEPTIDE, AND METHODS OF USE THEREOF
; FILE REFERENCE: N8289
; CURRENT APPLICATION NUMBER: US/10/094,240
; PRIOR FILING DATE: 2001-03-08
; PRIOR FILING DATE: 2002-01-24
; NUMBER OF SEQ ID NOS: 264,649
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 25
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Anopheles gambiae
US-10-094-240-25

```

Query Match

```

Best Local Similarity 51.8%; Score 1023; DB 14; Length 398;
Matches 204; Conservative 65; Mismatches 111; Indels 10; Gaps 7;
QY      1  MYVNFKVFKKCAPNGKVTLYMGRKDFVDHVSQVEPIDGIVLDEYIRDNKRVFGQIVCS 60
Db      1  MYVNFKVFKKCAPNGKVTLYMGRKDFVDHVSQVEPIDGIVLDEYIRDNKRVFGQIVCS 60
QY      61  FRYGREDEVMGKLFQKELCLASEQIYPRPEKSDKEQTKLQERLLKLGSAIPTFNIS 120
Db      61  FRYGREDEVMGKLFQKELCLASEQIYPRPEKSDKEQTKLQERLLKLGSAIPTFNIS 120
QY      121  PNAASSVTLLQOGEEDNDGDCGVSYVYKIFAGESEETDRTHRESVTLTGIRKIQFAPTKQOQ 180
Db      121  PNAASSVTLLQOGEEDNDGDCGVSYVYKIFAGESEETDRTHRESVTLTGIRKIQFAPTKQOQ 180
QY      179  RLPSSLSVSKFTFSQKINLVTLDREIYHGEKTAANIIVTNNRSKIKCPVVOHC 238
Db      179  RLPSSLSVSKFTFSQKINLVTLDREIYHGEKTAANIIVTNNRSKIKCPVVOHC 238
QY      239  EVTMV-NAQFSKHIALSEIREGCPITPGASFTKSFPLVPLASSNKDRGIALDGHLEDD 297
Db      239  EVTMV-NAQFSKHIALSEIREGCPITPGASFTKSFPLVPLASSNKDRGIALDGHLEDD 297
QY      298  VNLASSTLSECKCPDAMGIVISLRLKNCGLTGLGELQTDVPEFKLMNPAPGSVERER 357
Db      298  VNLASSTLSECKCPDAMGIVISLRLKNCGLTGLGELQTDVPEFKLMNPAPGSVERER 357
QY      357  VIHADSQADVETFRQDT--IDQASVDPE 383
Db      357  VIHADSQADVETFRQDT--IDQASVDPE 383
QY      358  VNALKKKKSIEHREYENSHYADDDNIVFE 387
Db      358  VNALKKKKSIEHREYENSHYADDDNIVFE 387

```

RESULT 4

```

; US-10-094-240-27
; Sequence 27, Application US/10094240
; Publication No. US20030082637A1
; GENERAL INFORMATION:
; APPLICANT: ZWIEBEL, LAURENCE J.
; TITLE OF INVENTION: ARRESTIN GENE, POLYPEPTIDE, AND METHODS OF USE THEREOF
; FILE REFERENCE: N8289
; CURRENT APPLICATION NUMBER: US/10/094,240
; PRIOR FILING DATE: 2001-03-08
; PRIOR FILING DATE: 2002-01-24
; NUMBER OF SEQ ID NOS: 264,649
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 27
; LENGTH 401
US-10-094-240-27

```


US-09-880-137-1
; Sequence 1, Application US/09880137
; Patent No. US20020031295A1
; GENERAL INFORMATION:
; APPLICANT: Berstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; FILE REFERENCE: MNI-131
; CURRENT APPLICATION NUMBER: US/09/880,137
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-880-137-1

Query Match
Best Local Similarity 45.8%; Score 903.5; DB 9; Length 418;
Matches 179; Conservative 76; Mismatches 112; Indels 13; Gaps 5;

QY 6 KVFKKCAPNGKVTLYMGKRDVNDHVSVEPIIDGIVLDDDEYIRDNKRVFGQIVCSFRYGR 65
DB 7 RVFKKASPNGLTIVYLGKRDVNDHVSVEPIIDGIVLDDDEYIRDNKRVFGQIVCSFRYGR 65
QY 66 EDEVMGILNFOKELCLASEQIYPRPEKSDKEQTKLOERLTKLGSNAIPFTFNISPNAPS 125
DB 66 EDLDVGLTFRKDLFVANVQSPFPAPEDKKPLTRLOERLTKLGEHAYPFTFEIPNLPC 125
QY 126 SVTLQGEDDNDGDPGVSYVYKIFAGESETDRTHRSSTVTLGIRKIQFAPTKGQOQPTL 125
DB 126 SVTLQGEDDNDGDPGVSYVYKIFAGESETDRTHRSSTVTLGIRKIQFAPTKGQOQPTL 125
QY 126 SVTLQGEDDNDGDPGVSYVYKIFAGESETDRTHRSSTVTLGIRKIQFAPTKGQOQPTL 125
DB 126 SVTLQGEDDNDGDPGVSYVYKIFAGESETDRTHRSSTVTLGIRKIQFAPTKGQOQPTL 125
QY 186 VRKDFMLSPGELEEVTLDKQLYLHGERIGVNICIRNNSNKMVKIKAMVQGVVDFVLFQ 185
DB 186 TTRQFLMSDKPLHLEASLDKEIYHGEPIISVNVHTNTNTKTKIKISVROYADICLFN 245
QY 246 NGSYRNTVASLETSEGCPIQPGSSLOKVMYLTPLSSNKGRIALDGOIKRQDOCLAST 245
DB 246 TAQYKCPVAMEADD--TVAPSSFTCKVYTLTPFLANNREKGLADGKLHEDTNLASS 303
QY 306 TLLAOPDORDAFGVITSYAVKVLFL--GALGELSA-----ELPVLNHPKPGTK---A 355
DB 304 TLLREGANREILGITIVSYKVKLVNKGGLGLDGLASSDVAVELPFTLHMPKPEEPHR 363
QY 356 KVIHADSOADVETFRQDTID 375
DB 364 EVPEHETPVDTNLIELDTND 383

RESULT 8
US-09-800-137A-1
; Sequence 1, Application US/09800137A
; Publication No. US20030157553A1
; GENERAL INFORMATION:
; APPLICANT: Berstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; FILE REFERENCE: MNI-131
; CURRENT APPLICATION NUMBER: US/09/800,137A
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-800-137A-1

Query Match
Best Local Similarity 45.8%; Score 903.5; DB 10; Length 418;
Matches 179; Conservative 76; Mismatches 112; Indels 13; Gaps 5;

QY 6 KVFKKCAPNGKVTLYMGKRDVNDHVSVEPIIDGIVLDDDEYIRDNKRVFGQIVCSFRYGR 65
DB 7 RVFKKASPNGLTIVYLGKRDVNDHVSVEPIIDGIVLDDDEYIRDNKRVFGQIVCSFRYGR 65
QY 66 EDEVMGILNFOKELCLASEQIYPRPEKSDKEQTKLOERLTKLGSNAIPFTFNISPNAPS 125
DB 66 EDLDVGLTFRKDLFVANVQSPFPAPEDKKPLTRLOERLTKLGEHAYPFTFEIPNLPC 125
QY 126 SVTLQGEDDNDGDPGVSYVYKIFAGESETDRTHRSSTVTLGIRKIQFAPTKGQOQPTL 125
DB 126 SVTLQGEDDNDGDPGVSYVYKIFAGESETDRTHRSSTVTLGIRKIQFAPTKGQOQPTL 125
QY 126 SVTLQGEDDNDGDPGVSYVYKIFAGESETDRTHRSSTVTLGIRKIQFAPTKGQOQPTL 125
DB 126 SVTLQGEDDNDGDPGVSYVYKIFAGESETDRTHRSSTVTLGIRKIQFAPTKGQOQPTL 125
QY 186 VRKDFMLSPGELEEVTLDKQLYLHGERIGVNICIRNNSNKMVKIKAMVQGVVDFVLFQ 185
DB 186 TTRQFLMSDKPLHLEASLDKEIYHGEPIISVNVHTNTNTKTKIKISVROYADICLFN 245
QY 246 NGSYRNTVASLETSEGCPIQPGSSLOKVMYLTPLSSNKGRIALDGOIKRQDOCLAST 245
DB 246 TAQYKCPVAMEADD--TVAPSSFTCKVYTLTPFLANNREKGLADGKLHEDTNLASS 303
QY 306 TLLAOPDORDAFGVITSYAVKVLFL--GALGELSA-----ELPVLNHPKPGTK---A 355
DB 304 TLLREGANREILGITIVSYKVKLVNKGGLGLDGLASSDVAVELPFTLHMPKPEEPHR 363
QY 356 KVIHADSOADVETFRQDTID 375
DB 364 EVPEHETPVDTNLIELDTND 383

RESULT 9
US-10-038-010-52
; Sequence 52, Application US/10038010
; Publication No. US20030040089A1
; GENERAL INFORMATION:
; APPLICANT: HYBRIGENICS
; TITLE OF INVENTION: Protein-protein interactions in adipocyte cells
; FILE REFERENCE: B4767A
; CURRENT APPLICATION NUMBER: US/10/038,010
; PRIOR FILING DATE: 2002-07-23
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: beta Arrestin 1
; LOCATION: (1)..(452)
; OTHER INFORMATION:
US-10-038-010-52

Query Match
Best Local Similarity 45.8%; Score 903.5; DB 14; Length 452;
Matches 179; Conservative 76; Mismatches 112; Indels 13; Gaps 5;

QY 6 KVFKKCAPNGKVTLYMGKRDVNDHVSVEPIIDGIVLDDDEYIRDNKRVFGQIVCSFRYGR 65
DB 7 RVFKKASPNGLTIVYLGKRDVNDHVSVEPIIDGIVLDDDEYIRDNKRVFGQIVCSFRYGR 65
QY 66 EDEVMGILNFOKELCLASEQIYPRPEKSDKEQTKLOERLTKLGSNAIPFTFNISPNAPS 125
DB 66 EDLDVGLTFRKDLFVANVQSPFPAPEDKKPLTRLOERLTKLGEHAYPFTFEIPNLPC 125
QY 126 SVTLQGEDDNDGDPGVSYVYKIFAGESETDRTHRSSTVTLGIRKIQFAPTKGQOQPTL 185
DB 126 SVTLQGEDDNDGDPGVSYVYKIFAGESETDRTHRSSTVTLGIRKIQFAPTKGQOQPTL 185

[illegible]

RESULT 10
US-10-043

```

; Sequence 348, Application US/10043487
; Publication No. US20030055220A1
; GENERAL INFORMATION:
; APPLICANT: HYBRIGENICS
; APPLICANT: Pierre, LEGRAIN
; TITLE OF INVENTION: Protein-protein interactions between Shigella flexneri polypeptides
; TITLE OF INVENTION: mammalian polypeptides
; FILE REFERENCE: B4778A
; CURRENT APPLICATION NUMBER: US/10/043,487
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/261,130
; PRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 561
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 348
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Shigella flexneri
US-10-043-487-348

```

Query Match	45.6%;	Score 900.5;	DB 14;	Length 418;
Best Local Similarity	46.8%;	Pred. No. 1.7e-75;		
Matches 178; Conservative	77;	Mismatches 112;	Indels 13;	Gaps 5;

[illegible]

```

RESULT 11
US-09-880-137-2
; Sequence 2, Application US/09880137
; Patent No. US20020031295A1
; GENERAL INFORMATION:
; APPLICANT: Berstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
; FILE REFERENCE: MNI-131
; CURRENT APPLICATION NUMBER: US/09/880,137
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186,706
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-137-2

```

Query Match	45.5%;	Score 897.5;	DB 9;	Length 418;
Best Local Similarity	46.8%;	Pred. No. 3.3e-75;		
Matches 178; Conservative	76;	Mismatches 113;	Indels 13;	Gaps 5;

QY	6	KVFEKKCAPNGKVTLLYMGKRDFVDHVSUVEPIDGIVLDDIYIRDNRKRVFGQIVCSFRGR	65
	:	: : : : : : : :	
DB	7	RVFKKASPNGLTVYL GKRFDFVDHIDLVPDVGVALVDP EYLKE -RRVVTLTCAFRYGR	65
QY	66	EEDDEVMGLNFOXELCLASEQIYPPEBKS DKEQTLOERLLKLGSNAIPFTENISPNAS	125
	:	: : : : :	
DB	66	EDLDVLGLTFRXDLFVANQSFPAPBEDKKPLTRIOERLI KLG ENAYPFTFEIPRNLC	125
QY	126	SVTLQQGEDNDGDCGVSYVKI PAGESETDRTHRSTVLTIGRIQFAPTKGQOPCTL	185
	:	: : : : : : : :	
DB	126	SVTLQGPEDGTGACGV DYEVKAFC AENLEEKIHKN SVRLVIRKVYA PERGPQTAE	185
QY	186	VAKDFMLSPGELEVTLDKQLYHERIGVNICIRNSSNMKVKKIKAMVQQGV DVVLFQ	245
	:	: : : : : : : : : : : : : : : : : : :	
DB	186	TTRQFLMSDKPLHL EASLDKEIYHGEPIS VNVHYNTNTNKTVKKIKISVRQADICLEFN	245
QY	246	NCSYRNTVASLETSEGCPIQPGSS LQKMVYLP LLSSNKRGI ALDGQIKRODOCIAS T	305
	:	: : : :	
DB	246	TAOYKCPVAMEEADD--TVAPSSTFC KYVTLTPFLANNREKRGLALDGKLKHEDTNLASS	303
QY	306	TLLAQPDQRDAFGVII SYAVKYLF--LGALGGELSA-----ELPFVLMHPKP GTK---A	355
	:	: : : : : : : : : : : : : : : : : : :	
DB	304	TLLREGANREITGIIVSYKVKVLYVESRGGLGLDLASSDVAVELPFTLMHPKPKEEFHR	363
QY	356	KVIHADSQADVETFRQDTID	375
	:	: : : : : : : : : : : : : : : : : : : :	
DB	364	EVPENETPVDTNLIELDTND	383

RESULT 12

```

US-09-800-137A-2
; Sequence 2, Application US/09800137A
; Publication No. US20030157553A1
; GENERAL INFORMATION:
; APPLICANT: Berstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
; FILE REFERENCE: NMT-131
; CURRENT APPLICATION NUMBER: US/09/800,137A
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186,706
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 418
; TYPE: PR

```


ORGANISM: Homo sapiens
US-09-800-137A-2

Query Match

Best Local Similarity 45.5%; Score 897.5; DB 10; Length 418;
Matches 178; Conservative 76; Mismatches 113; Indels 13; Gaps 5;

QY 6 KVFKKCAPNGKVTLYMGKRDVHDVHSGVEPIDGIVLDDDEYIRDNKKVFGQIVCSFRYGR 65
DB 7 RVFKKASPNKLTIVYLGKRDVHDVHSGVEPIDGIVLDDDEYIRDNKKVFGQIVCSFRYGR 65
QY 66 EEDVWGLNFQKELCLASEQIYPRPEKSDKEQTKLOERLKLGSNAIPFTENISPNAPS 125
DB 66 EDLDVLGLTFRKDLFVAVVQSPAPEDKPELTRLQERLKLGEHAYPFTFELPPLPC 125
QY 126 SVTLQGEDNDGDPGCVSYVYKIFAGESETDRTHRSSTVTLGIRKIOFAPTKOGQOPCTL 185
DB 126 SVTLQGEDNDGDPGCVSYVYKIFAGESETDRTHRSSTVTLGIRKIOFAPTKOGQOPCTL 185
QY 186 VRKDFMLSPGELLEVTLDDKQLYLHGERIGVNICIRNNSNMKVKIKAMVQGVVVLFFQ 245
DB 186 TTRQFLMSDKPLHLASLDKELYHGEPIVSVNHTNNTKTKIKISVRQYADICLFS 245
QY 246 NSGYRNTVASLETSEGCPIQPGSSLOKVMYLTPLSSNKGRIALDGOIKRQDQCLAST 305
DB 246 TAQYKCPVAQLEODD--QVSPSTFCVYITPLPLSSNKGRIALDGOIKRQDQCLAST 305
QY 306 TLLAQPDQDAFGVIISAVKVLFLGALGELSAELPFLVLMHPKP 351
DB 306 TLLAQPDQDAFGVIISAVKVLFLGALGELSAELPFLVLMHPKP 351
QY 304 TLLREGANREILGIIVSYKVKLVESRGGLLGLASSDAVELPFTLMDHPKPEPPHR 363
DB 304 TLLREGANREILGIIVSYKVKLVESRGGLLGLASSDAVELPFTLMDHPKPEPPHR 363
QY 356 KVIHADQADVETFRQDTID 375
DB 356 EVPENETPVDNLIELDTND 383

RESULT 13

US-09-880-137-8
Sequence 8, Application US/09880137
Patent No. US20020031295A1
GENERAL INFORMATION:
APPLICANT: Berstein, Gabriel
TITLE OF INVENTION: METHODS OF ASSAYING FOR G
FILE REFERENCE: MNI-131
CURRENT APPLICATION NUMBER: US/09/880,137
PRIOR FILING DATE: 2001-03-05
PRIORITY APPLICATION NUMBER: US 60/186,706
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
LENGTH: 382
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Homo sapiens mutation
US-09-880-137-8

Query Match

Best Local Similarity 44.9%; Score 885; DB 9; Length 382;
Matches 167; Conservative 77; Mismatches 98; Indels 4; Gaps 3;

QY 6 KVFKKCAPNGKVTLYMGKRDVHDVHSGVEPIDGIVLDDDEYIRDNKKVFGQIVCSFRYGR 65
DB 8 RVFKKASPNKLTIVYLGKRDVHDVHSGVEPIDGIVLDDDEYIRDNKKVFGQIVCSFRYGR 65
QY 66 EEDVWGLNFQKELCLASEQIYPRPEKSDKEQTKLOERLKLGSNAIPFTENISPNAPS 125
DB 66 EDLDVLGLTFRKDLFVAVVQSPAPEDKPELTRLQERLKLGEHAYPFTFELPPLPC 125
QY 126 SVTLQGEDNDGDPGCVSYVYKIFAGESETDRTHRSSTVTLGIRKIOFAPTKOGQOPCTL 185
DB 126 SVTLQGEDNDGDPGCVSYVYKIFAGESETDRTHRSSTVTLGIRKIOFAPTKOGQOPCTL 185

us-10-056-405-2.rapb

DB 127 SVTLQGEDNDGDPGCVSYVYKIFAGESETDRTHRSSTVTLGIRKIOFAPTKOGQOPCTL 185
QY 186 VRKDFMLSPGELLEVTLDDKQLYLHGERIGVNICIRNNSNMKVKIKAMVQGVVVLFFQ 245
DB 187 TTRHFLMSDRSLHLASLDKELYHGEPIVSVNHTNNTKTKIKISVRQYADICLFS 245
QY 246 NSGYRNTVASLETSEGCPIQPGSSLOKVMYLTPLSSNKGRIALDGOIKRQDQCLAST 305
DB 247 TAQYKCPVAQLEODD--QVSPSTFCVYITPLPLSSNKGRIALDGOIKRQDQCLAST 305
QY 306 TLLAQPDQDAFGVIISAVKVLFLGALGELSAELPFLVLMHPKP 351
DB 306 TLLAQPDQDAFGVIISAVKVLFLGALGELSAELPFLVLMHPKP 351
QY 305 TIVGANKVGLIIVSYKVKLVESRGGLLGLASSDAVELPFTLMDHPKPEPPHR 363
DB 305 TIVGANKVGLIIVSYKVKLVESRGGLLGLASSDAVELPFTLMDHPKPEPPHR 363

RESULT 14

US-09-800-137A-8
Sequence 8, Application US/09800137A
Patent No. US20030157553A1
GENERAL INFORMATION:
APPLICANT: Berstein, Gabriel
TITLE OF INVENTION: METHODS OF ASSAYING FOR G
FILE REFERENCE: MNI-131
CURRENT APPLICATION NUMBER: US/09/800,137A
PRIOR FILING DATE: 2001-03-05
PRIORITY APPLICATION NUMBER: US 60/186,706
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
LENGTH: 382
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Homo sapiens mutation
US-09-800-137A-8

Query Match

Best Local Similarity 44.9%; Score 885; DB 10; Length 382;
Matches 167; Conservative 77; Mismatches 98; Indels 4; Gaps 3;

QY 6 KVFKKCAPNGKVTLYMGKRDVHDVHSGVEPIDGIVLDDDEYIRDNKKVFGQIVCSFRYGR 65
DB 8 RVFKKASPNKLTIVYLGKRDVHDVHSGVEPIDGIVLDDDEYIRDNKKVFGQIVCSFRYGR 65
QY 66 EEDVWGLNFQKELCLASEQIYPRPEKSDKEQTKLOERLKLGSNAIPFTENISPNAPS 125
DB 66 EDLDVLGLTFRKDLFVAVVQSPAPEDKPELTRLQERLKLGEHAYPFTFELPPLPC 125
QY 126 SVTLQGEDNDGDPGCVSYVYKIFAGESETDRTHRSSTVTLGIRKIOFAPTKOGQOPCTL 185
DB 126 SVTLQGEDNDGDPGCVSYVYKIFAGESETDRTHRSSTVTLGIRKIOFAPTKOGQOPCTL 185
QY 186 VRKDFMLSPGELLEVTLDDKQLYLHGERIGVNICIRNNSNMKVKIKAMVQGVVVLFFQ 245
DB 187 TTRHFLMSDRSLHLASLDKELYHGEPIVSVNHTNNTKTKIKISVRQYADICLFS 245
QY 246 NSGYRNTVASLETSEGCPIQPGSSLOKVMYLTPLSSNKGRIALDGOIKRQDQCLAST 305
DB 247 TAQYKCPVAQLEODD--QVSPSTFCVYITPLPLSSNKGRIALDGOIKRQDQCLAST 305
QY 306 TLLAQPDQDAFGVIISAVKVLFLGALGELSAELPFLVLMHPKP 351
DB 306 TLLAQPDQDAFGVIISAVKVLFLGALGELSAELPFLVLMHPKP 351
QY 305 TIVGANKVGLIIVSYKVKLVESRGGLLGLASSDAVELPFTLMDHPKPEPPHR 363
DB 305 TIVGANKVGLIIVSYKVKLVESRGGLLGLASSDAVELPFTLMDHPKPEPPHR 363

RESULT 15

US-09-880-137-4
Sequence 4, Application US/09880137
Patent No. US20020031295A1
GENERAL INFORMATION:
APPLICANT: Berstein, Gabriel


```

; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
; FILE REFERENCE: MNI-131
; CURRENT APPLICATION NUMBER: US/09/880,137
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186,706
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-137-4

```

Query Match	44.9%;	Score 885;	DB 9;	Length 409;
Best Local Similarity	48.3%;	Pred. No. 4.7e-74;		
Matches 167;	Conservative 77;	Mismatches 98;	Indels 4;	Gaps 3;

[illegible]

Search completed: February 9, 2005, 23:44:23
Job time : 132 secs

This Page Blank (uspto)

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 9, 2005, 23:45:38 / Search time 165 seconds
(without alignments)
897.753 Million cell updates/sec

Title: US-10-056-405-2

Perfect score: 383
Sequence: 1 MVTNFKVFKKCAPNGKVTLY.....ADVETFRQDTIDQCASVDPE 383

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	383	100.0	383	5 ABP52833	Abp52833 Anopheles
2	383	100.0	383	7 ABR84476	ABR84476 Mosquito
3	20	5.2	364	4 ABB61736	Abb61736 Drosophila
4	20	5.2	364	8 ADQ89588	Adq89588 Antagonis
5	11	2.9	382	4 AAG67785	Aag67785 An exempl
6	11	2.9	398	7 ABR84484	ABR84484 Mosquito
7	11	2.9	401	4 ABB61964	Abb61964 Drosophila
8	11	2.9	409	4 AAG67784	Aag67784 An exempl
9	11	2.9	409	4 AAG67781	Aag67781 Amino aci
10	11	2.9	409	7 ADE58183	Ade58183 Human pro
11	11	2.9	409	7 ADE58179	Ade58179 Human pro
12	11	2.9	409	7 ADN95251	Adn95251 Human BEC
13	11	2.9	410	5 ABG69496	Abg69496 Rat bait
14	11	2.9	410	7 ADE58177	Ade58177 Rat Prote
15	11	2.9	410	7 ADE58181	Ade58181 Rat Prote
16	11	2.9	526	8 ADR23187	Adr23187 Yellow flu
17	11	2.9	526	8 ADR23188	Adr23188 Green flu
18	11	2.9	526	8 ADR23186	Adr23186 Yellow fl
19	9	2.3	388	4 AAG67782	Aag67782 Amino aci
20	9	2.3	388	4 AAG67783	Aag67783 Amino aci
21	9	2.3	470	4 ABB58174	Abb58174 Drosophila
22	8	2.1	22	7 ADJ94231	Adj94231 Self-anti
23	8	2.1	38	4 AAM20580	Aam20580 Peptide #
24	8	2.1	38	4 ABB41697	Abb41697 Peptide #
25	8	2.1	38	4 AAM35493	Aam35493 Peptide #

26	8	2.1	38	4 ABB25470	Abb25470 Protein #
27	8	2.1	38	4 AAM75381	Aam75381 Human bon
28	8	2.1	38	4 AAM62570	Aam62570 Human bra
29	8	2.1	38	4 ABG57138	Abg57138 Human liv
30	8	2.1	38	5 ABG44975	Abg44975 Human pep
31	8	2.1	180	6 ADA00634	Ada00634 Human bet
32	8	2.1	182	7 ADD27419	Add27419 Human adi
33	8	2.1	182	7 ADD27127	Add27127 Human adi
34	8	2.1	182	7 ADD27197	Add27197 Human adi
35	8	2.1	187	6 ABU70623	Abu70623 Human adi
36	8	2.1	187	7 ADD27507	Add27507 Human adi
37	8	2.1	204	2 AAW20559	Aaw20559 Helicobac
38	8	2.1	204	2 AAW24688	Aaw24688 H. pylori
39	8	2.1	212	4 AAG73899	Aag73899 Human col
40	8	2.1	279	7 ABO78668	AbO78668 Pseudomon
41	8	2.1	315	6 ADA00636	Ada00636 Human bet
42	8	2.1	360	6 ADA00635	Ada00635 Human bet
43	8	2.1	366	2 AAW20643	Aaw20643 H. pylori
44	8	2.1	369	4 ABG13574	Abg13574 Novel hum
45	8	2.1	405	4 AAM78763	Aam78763 Human pro

ALIGNMENTS

RESULT 1	
ABP52833	ABP52833 standard; protein; 383 AA.
ID	ABP52833;
AC	ABP52833;
XX	
DT	01-NOV-2002 (first entry)
XX	
DE	Anopheles gambiae arrestin 1 protein SEQ ID NO:2.
XX	
KW	Anopheles gambiae; mosquito; olfactory gene; arrestin 1; pest control;
KW	odourant receptor; olfaction.
XX	
OS	Anopheles gambiae.
XX	
PN	WO200259274-A2.
XX	
PD	01-AUG-2002.
XX	
PF	28-JAN-2002; 2002WO-US002549.
XX	
PR	26-JAN-2001; 2001US-0264649P.
PR	24-JAN-2002; 2002US-00056405.
XX	
PA	(UYVA-) UNIV VANDERBILT.
XX	
PI	Zwiebel LJ;
XX	
DR	WPI; 2002-627421/67.
DR	N-PSDB; ABQ75102.
XX	
PT	New mosquito olfaction polypeptides and polynucleotides, useful for
PT	mosquito management, i.e. controlling the pest and disease vectors, or
PT	for identifying pest control agents.
XX	
PS	Claim 18; Fig 2; 96pp; English.
XX	
CC	The present invention describes a purified Anopheles gambiae olfaction
CC	polypeptide comprising a 383, 394, 380, 411, 412, 391, 157 or 401 residue
CC	amino acid sequence (see ABP52833 to ABP52840) (S1), a conservatively
CC	modified amino acid sequence of them, or a sequence of (S1) with at least
CC	20 consecutive residues. Also described: (1) an isolated polynucleotide
CC	comprising: (a) a nucleotide sequence encoding the purified Anopheles
CC	gambiae olfaction polypeptide; or (b) a nucleotide sequence that
CC	hybridises under stringent conditions to a hybridisation probe comprising
CC	a 1964, 1239, 1142, 1236, 1194, 1176, 474 or 1206 nucleotide sequence
CC	(see ABQ75102 to ABQ75105 and ABQ75110 to ABQ75113) (S2), or its
CC	complement; and (2) a method for identifying an agent that binds to

CC mosquito olfaction molecules comprising: (a) providing an isolated
CC mosquito olfaction molecule; (b) contacting a test agent with the
CC isolated mosquito olfaction molecule; and (c) detecting specific binding
CC of the test agent to the isolated mosquito olfaction molecule, where the
CC presence of specific binding identifies the test agent as a mosquito
CC olfaction-binding compound. The mosquito olfaction molecules are useful
CC for mosquito management, i.e. controlling this pest and disease vector
CC method from the present invention of screening for substances that
CC modulate arrestin-odourant receptor interaction for useful for identifying
CC pest control agents. The present sequence represents Anopheles gambiae
CC arrestin 1 from the present invention
XX
SQ Sequence 383 AA;

Query Match
Best Local Similarity 100.0%; Score 383; DB 5; Length 383;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVTNFKVFKKCAPNGKVTLYMGKRDVDFVHSGVEPIDGIVLDEYIRDNKRVFGQIVCS 60
DB 1 MVTNFKVFKKCAPNGKVTLYMGKRDVDFVHSGVEPIDGIVLDEYIRDNKRVFGQIVCS 60
QY 61 FRYGREDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKLGSNAPFTFNIS 120
DB 61 FRYGREDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKLGSNAPFTFNIS 120
QY 121 PNAPSSVTLLQGGEDNDGPGCVSYVYKIFAGESETDRTTHRSSTVTLGIRKIQFAPTKQG 180
DB 121 PNAPSSVTLLQGGEDNDGPGCVSYVYKIFAGESETDRTTHRSSTVTLGIRKIQFAPTKQG 180
QY 181 OPTLVKRDPMFLSPGELLEVTLTKQLYLHGERIGVNICIRNSNKNVKKIKAMVQGVND 240
DB 181 OPTLVKRDPMFLSPGELLEVTLTKQLYLHGERIGVNICIRNSNKNVKKIKAMVQGVND 240
QY 241 VVLFONGSYRNTVASLETSEGCPIQPGSSLOKVMYLTPLSSNKRGRGIALDGOIKRQDQ 300
DB 241 VVLFONGSYRNTVASLETSEGCPIQPGSSLOKVMYLTPLSSNKRGRGIALDGOIKRQDQ 300
QY 301 CLASTTLLAQPDPORDAFGVIIISYAVKVLFLGALGELSALPFLVLMHPKPGTKAKVIHA 360
DB 301 CLASTTLLAQPDPORDAFGVIIISYAVKVLFLGALGELSALPFLVLMHPKPGTKAKVIHA 360
QY 361 DSQADVETFRQDTIDQASVDPE 383
DB 361 DSQADVETFRQDTIDQASVDPE 383

RESULT 2
ID ABR84476 standard; protein; 383 AA.
XX ABR84476;
AC ABR84476;
XX
DT 15-JAN-2004 (first entry)
XX
DE Mosquito olfaction molecule, arrestin 1.
XX
KW Arrestin 1; mosquito; olfaction; insecticide; antimalarial.
XX
OS Anopheles gambiae.
XX
PN WO2003076590-A2.
XX
PD 18-SEP-2003.
XX
PF 10-MAR-2003; 2003WO-US007174.
XX
PR 08-MAR-2002; 2002US-00094240.
XX
PA (UYVA-) UNIT VANDERBILT.
XX
PI Zwiebel LJ;
XX

DR WPI; 2003-722331/68.
DR N-PSDB; ACF79716.
XX
PT New mosquito arrestin 1 and 2 genes and polypeptides, useful for
PT identifying mosquito olfaction molecule binding compounds which reduce
PT the ability of mosquitoes to locate sources of bloodmeal, e.g. humans.
XX
PS Claim 1; Fig 2; 101p; English.
XX
CC The present sequence is the protein sequence of arrestin 1, a novel
CC mosquito olfaction molecule. The invention provides 9 novel mosquito
CC polypeptides and the nucleic acids encoding them. These are arrestin 1
CC and 2 and odorant receptor molecules 1-7. The odorant receptors function
CC in a ligand-induced signal transduction pathway for the activation of
CC mosquito olfaction. Arrestin functions to inhibit the activation of
CC transduction cascade. Thus, the odorant receptors act as an 'on' switch
CC and arrestin as an 'off' switch for the odorant receptors function
CC mosquito. Methods are provided for identifying compounds that interfere
CC with the operation of the mosquito olfactory system, particularly
CC compounds that modulate arrestin 2 activity. These are useful for the
CC control of mosquitoes, particularly by reducing their ability to locate
CC sources of bloodmeal
XX
SQ Sequence 383 AA;

Query Match
Best Local Similarity 100.0%; Score 383; DB 7; Length 383;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVTNFKVFKKCAPNGKVTLYMGKRDVDFVHSGVEPIDGIVLDEYIRDNKRVFGQIVCS 60
DB 1 MVTNFKVFKKCAPNGKVTLYMGKRDVDFVHSGVEPIDGIVLDEYIRDNKRVFGQIVCS 60
QY 61 FRYGREDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKLGSNAPFTFNIS 120
DB 61 FRYGREDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKLGSNAPFTFNIS 120
QY 121 PNAPSSVTLLQGGEDNDGPGCVSYVYKIFAGESETDRTTHRSSTVTLGIRKIQFAPTKQG 180
DB 121 PNAPSSVTLLQGGEDNDGPGCVSYVYKIFAGESETDRTTHRSSTVTLGIRKIQFAPTKQG 180
QY 181 OPTLVKRDPMFLSPGELLEVTLTKQLYLHGERIGVNICIRNSNKNVKKIKAMVQGVND 240
DB 181 OPTLVKRDPMFLSPGELLEVTLTKQLYLHGERIGVNICIRNSNKNVKKIKAMVQGVND 240
QY 241 VVLFONGSYRNTVASLETSEGCPIQPGSSLOKVMYLTPLSSNKRGRGIALDGOIKRQDQ 300
DB 241 VVLFONGSYRNTVASLETSEGCPIQPGSSLOKVMYLTPLSSNKRGRGIALDGOIKRQDQ 300
QY 301 CLASTTLLAQPDPORDAFGVIIISYAVKVLFLGALGELSALPFLVLMHPKPGTKAKVIHA 360
DB 301 CLASTTLLAQPDPORDAFGVIIISYAVKVLFLGALGELSALPFLVLMHPKPGTKAKVIHA 360
QY 361 DSQADVETFRQDTIDQASVDPE 383
DB 361 DSQADVETFRQDTIDQASVDPE 383

RESULT 3
ID ABB61736 standard; protein; 364 AA.
XX ABB61736;
AC ABB61736;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 12000.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical.
XX
OS Drosophila melanogaster.
XX

PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
XX 11-JUL-2000; 2000US-00614150.
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
DR N-PSDB; ABL05839.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
PS Disclosure; SEQ ID NO 12000; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 364 AA;

Query Match 5.2%; Score 20; DB 4; Length 364;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 228 VKKIKAMVQGVDVVLFGNG 247
|||
DB 227 VKKIKAMVQGVDVVLFGNG 246

RESULT 4
ADQ89588
ID ADQ89588 standard; protein; 364 AA.
XX
AC ADQ89588;

DT 21-OCT-2004 (first entry)
XX

DE Antagonist of cell cycle progression polypeptide #9.

XX
KW Cytostatic; cancer; cell division cycle; mitosis; meiosis;
KW cell cycle progression.
XX

OS Drosophila melanogaster.
XX

PN WO2004063362-A2.
XX

PD 29-JUL-2004.
XX

PF 31-DEC-2003; 2003WO-GB005635.
XX

PR 10-JAN-2003; 2003US-0439123P.
PR 06-MAY-2003; 2003US-0468402P.
XX

PA (CYCL-) CYCLACEL LTD.
XX

PI Glover D, Bell G, Frenz L, Midgley C;
XX

DR WPI; 2004-544089/52.

DR N-PSDB; ADQ89587.
XX
XX New cell cycle progression genes and proteins for modulating cell cycle
PT progression in cells, for preventing, treating or diagnosing cell
PT proliferative diseases (e.g. cancer) or for identifying modulators of
PT mitosis or meiosis.
XX
PS Claim 2; SEQ ID NO 18; 461pp; English.
XX

CC The present invention relates to a polynucleotide for preventing,
CC treating or diagnosing a disease in an individual. The composition or the
CC polypeptide, polynucleotide or RNA precursor, or antibody is useful for
CC diagnosing, preventing or treating diseases (e.g. cell proliferative
CC diseases such as cancer) in an individual. These may also be used for
CC identifying substances capable of binding to or modulating the function
CC of the polypeptide, capable of affecting the function of the
CC corresponding gene, or capable of inhibiting the cell division cycle or
CC cell cycle progression, preferably mitosis and/or meiosis. The present
CC sequence represents an antagonist of cell cycle progression protein
CC sequence.
XX
SQ Sequence 364 AA;

Query Match 5.2%; Score 20; DB 8; Length 364;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 228 VKKIKAMVQGVDVVLFGNG 247
|||
DB 227 VKKIKAMVQGVDVVLFGNG 246

RESULT 5
AAG67785
ID AAG67785 standard; protein; 382 AA.
XX
AC AAG67785;

DT 10-DEC-2001 (first entry)
XX

DE An exemplary phosphorylation-independent arrestin mutant.

XX
KW Arrestin; phosphorylation-independent arrestin mutant;
KW G protein-coupled receptor; GPCR; GPCR ligand; retinitis pigmentosa;
KW stationary night blindness; colour blindness; nephrogenic DI;
KW isolated glucocorticoid deficiency; hyperfunctioning thyroid adenoma;
KW familial hypocalcaemic hypercalcaemia; hyperparathyroidism;
KW neurological disorder.
XX

OS Unidentified.
XX

PN WO200167106-A2.
XX

PD 13-SEP-2001.
XX

PF 05-MAR-2001; 2001WO-US007304.
XX

PR 03-MAR-2000; 2000US-0186706P.
XX

PA (MILL-) MILLENNIUM PHARM INC.
XX

PI Bernstein G;
XX

DR WPI; 2001-602637/68.
XX

PT Identifying a G protein-coupled receptor ligand, useful for treating e.g.
PT retinitis pigmentosa, color blindness or neurological disorders, uses
PT phosphorylation-independent arrestin mutants particularly suited for in
PT vitro screening assays.
XX
XX

PS Disclosure; Page 47; 47pp; English.
XX

CC The present sequence represents an exemplary phosphorylation-independent

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 62 RYGREDEVMG 72
 |||||
 Db 61 RYGREDEVMG 71

RESULT 8
 AAG67784
 ID AAG67784 standard; protein; 409 AA.

AC AAG67784;

DT 10-DEC-2001 (first entry)

DE An exemplary phosphorylation-independent arrestin mutant.

XX Arrestin; phosphorylation-independent arrestin mutant;
 KW G protein-coupled receptor; GPCR; GPCR ligand; retinitis pigmentosa;
 KW stationary night blindness; colour blindness; nephrogenic DI;
 KW isolated glucocorticoid deficiency; hyperfunctioning thyroid adenoma;
 KW familial hypocalcemic hypercalcemia; hyperparathyroidism;
 KW neurological disorder.

OS Unidentified.

PN WO200167106-A2.

PD 13-SEP-2001.

PF 05-MAR-2001; 2001WO-US007304.

PR 03-MAR-2000; 2000US-0186706P.

PA (MILL-) MILLENNIUM PHARM INC.

PI Berstein G;

DR WPI; 2001-602637/68.

PT Identifying a G protein-coupled receptor ligand, useful for treating e.g.
 PT retinitis pigmentosa, color blindness or neurological disorders, uses
 PT phosphorylation-independent arrestin mutants particularly suited for in
 PT vitro screening assays.
 PS Disclosure; Page 47; 47pp; English.

XX The present sequence represents an exemplary phosphorylation-independent
 CC arrestin mutant. Such mutants are used in screening assays to identify
 CC ligands and/or modulators of G protein-coupled receptors (GPCRs). A
 CC method for identifying a GPCR ligand comprises contacting a composition
 CC comprising the GPCR and a constitutively active arrestin mutant with a
 CC test compound; and determining the ability of the test compound to
 CC modulate binding of arrestin mutant to the GPCR, where modulation of
 CC binding indicates that the test compound is a GPCR ligand. The method is
 CC used for identifying potential ligands and/or modulators of GPCRs,
 CC particularly modulators, for use as human therapeutics. Modulators of
 CC GPCR may be used for treating patients having e.g. retinitis pigmentosa,
 CC stationary night blindness, colour blindness, nephrogenic DI, isolated
 CC glucocorticoid deficiency, hyperfunctioning thyroid adenomas, familial
 CC hypocalcemic hypercalcemia, hyperparathyroidism and neurological
 CC disorders. The methods may be used for screening pluralities of test
 CC compounds (e.g. a small molecule library of compounds) or a composition
 CC containing a plurality of GPCRs. The methods may be used in screening
 CC assays for identification of natural and surrogate agonists of orphan
 CC GPCRs, and for identification of GPCR antagonists and/or agonists
 XX Sequence 409 AA;

Query Match 2.9%; Score 11; DB 4; Length 409;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 341 ELPFVLMHPKP 351
 |||||
 Db 339 ELPFVLMHPKP 349

RESULT 9
 AAG67781

ID AAG67781 standard; protein; 409 AA.

AC AAG67781;

DT 10-DEC-2001 (first entry)

DE Amino acid sequence of human beta-arrestin 2.

XX Arrestin; phosphorylation-independent arrestin mutant;
 KW G protein-coupled receptor; GPCR; GPCR ligand; retinitis pigmentosa;
 KW stationary night blindness; colour blindness; nephrogenic DI;
 KW isolated glucocorticoid deficiency; hyperfunctioning thyroid adenoma;
 KW familial hypocalcemic hypercalcemia; hyperparathyroidism;
 KW neurological disorder.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Region 156..185
 /note="putative phosphorylation-recognition region"

PN WO200167106-A2.

PD 13-SEP-2001.

PF 05-MAR-2001; 2001WO-US007304.

PR 03-MAR-2000; 2000US-0186706P.

PA (MILL-) MILLENNIUM PHARM INC.

PI Berstein G;

DR WPI; 2001-602637/68.

PT Identifying a G protein-coupled receptor ligand, useful for treating e.g.
 PT retinitis pigmentosa, color blindness or neurological disorders, uses
 PT phosphorylation-independent arrestin mutants particularly suited for in
 PT vitro screening assays.
 PS Disclosure; Page 46; 47pp; English.

XX The present sequence represents an arrestin protein. The specification
 CC describes phosphorylation-independent arrestin mutants. These mutants are
 CC used in screening assays to identify ligands and/or modulators of G
 CC protein-coupled receptors (GPCRs). A method for identifying a GPCR ligand
 CC comprises contacting a composition comprising the GPCR and a
 CC constitutively active arrestin mutant with a test compound; and
 CC determining the ability of the test compound to modulate binding of
 CC arrestin mutant to the GPCR, where modulation of binding indicates that
 CC the test compound is a GPCR ligand. The method is used for identifying
 CC potential ligands and/or modulators of GPCRs, particularly modulators,
 CC for use as human therapeutics. Modulators of GPCR may be used for
 CC treating patients having e.g. retinitis pigmentosa, stationary night
 CC blindness, colour blindness, nephrogenic DI, isolated glucocorticoid
 CC deficiency, hyperfunctioning thyroid adenomas, familial hypocalcemic
 CC hypercalcemia, hyperparathyroidism and neurological disorders. The
 CC methods may be used for screening pluralities of test compounds (e.g. a
 CC small molecule library of compounds) or a composition containing a
 CC plurality of GPCRs. The methods may be used in screening assays for
 CC identification of natural and surrogate agonists of orphan GPCRs, and for
 CC identification of GPCR antagonists and/or agonists
 XX Sequence 409 AA;

Query Match 2.9%; Score 11; DB 4; Length 409;

Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 341 ELPFVLMHPKP 351
DB 339 ELPFVLMHPKP 349

RESULT 10

AD58183
ID ADE58183 standard; protein; 409 AA.
AC ADE58183;
XX
XX
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein P32121, SEQ ID NO 4054.

XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
XX spared nerve injury; SNI; Chung.
OS Homo sapiens.
XX
XX
PN WO2003016475-A2.
XX
XX
PD 27-FEB-2003.
XX
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
DR WPI; 2003-268312/26.
DR GENBANK; P32121.
XX
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
XX
PS Claim 1; Page; 1017pp; English.

CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 409 AA;

Query Match
Best Local Similarity 2.9%; Score 11; DB 7; Length 409;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 341 ELPFVLMHPKP 351
DB 339 ELPFVLMHPKP 349

RESULT 11

AD58179
ID ADE58179 standard; protein; 409 AA.
AC ADE58179;
XX
XX
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein P32121, SEQ ID NO 4050.

XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
XX spared nerve injury; SNI; Chung.
OS Homo sapiens.
XX
XX
PN WO2003016475-A2.
XX
XX
PD 27-FEB-2003.
XX
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
DR WPI; 2003-268312/26.
DR GENBANK; P32121.
XX
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
XX
PS Claim 1; Page; 1017pp; English.

CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction

CC injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 409 AA;

Query Match 2.9%; Score 11; DB 7; Length 409;

Best Local Similarity 100.0%; Pred. No. 0.11;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 341 ELPFVLMHPKP 351

Db 339 ELPFVLMHPKP 349

RESULT 12

ADN95251

ID ADN95251 standard; protein; 409 AA.

XX AC ADN95251;

XX DT 01-JUL-2004 (first entry)

XX DE Human BHC/LEC-related protein sequence SegID173.

XX growth; differentiation; blood endothelial cell; BEC;
KW lymphatic endothelial cell; LEC; hereditary lymphoedema; VEGF-3;
KW lymphatic growth agent; VEGF-C; VEGF-D; antiangiogenic; cyostatic;
KW vasotropic; antiinflammatory; gene therapy; endothelial cell disorder;
KW inflammatory disease; cancer metastasis; lymphatic system; human.

OS Homo sapiens.
XX WO2003080640-A1.
XX PN 02-OCT-2003.
XX PD 07-MAR-2003; 2003WO-US006900.
XX PF 07-MAR-2002; 2002US-0363019P.
XX PR (LUDW-) LUDWIG INST CANCER RES.
XX PA (LICN) LICENTIA LTD.
XX PI Alitalo K, Makinen T, Petrova T, Saharinen P, Saharinen J;
XX PI WPI; 2003-876899/81.
XX DR N-PSDB; ADN95252.

XX PS Example 1; SEQ ID NO 173; 176pp; English.
XX This invention relates to a method of differentially modulating the
CC growth or differentiation of blood endothelial cells (BEC) or lymphatic
CC endothelial cells (LEC) comprises contacting endothelial cells with a
CC composition comprising an agent that differentially modulates blood or
CC lymphatic endothelial cells. Treating hereditary lymphoedema comprises
CC identifying a human subject with lymphoedema and with a mutation in at
CC least one allele of a gene encoding a LEC protein, where the mutation
CC correlates with lymphoedema in human subjects, and with the proviso that
CC the LEC protein is not VEGF-3; and administering to the subject a
CC composition comprising a lymphatic growth agent selected from VEGF-C or
CC VEGF-D polypeptides and polynucleotides. The invention may be useful for
CC the development of compounds with an antiangiogenic, cyostatic,
CC vasotropic or antiinflammatory activity or for gene therapy. The method
CC is useful in modulating the growth or differentiation of blood
CC endothelial cells or lymphatic endothelial cells, in treating hereditary
CC lymphoedema, in screening for an endothelial cell disorder or
CC predisposition to the disorder or in monitoring the efficacy or toxicity
CC of a drug on endothelial cells. The agent is useful in manufacturing a
CC medicament for the differential modulation of blood vessel endothelial

CC cell or lymphatic vessel endothelial cell growth or differentiation. The
CC lymphatic growth agent may also be used in manufacturing a medicament for
CC the treatment of hereditary lymphoedema resulting from a mutation in a
CC LEC gene or of other diseases involving the lymphatic vessels, such as
CC various inflammatory diseases and cancer metastasis via the lymphatic
CC system. The present sequence is that of a human LEC/BEC differentially
CC expressed protein which is related to the method of the invention. Note:
CC This sequence does not appear in the specification but was obtained by
CC the indexer using the source data given in table 14 of the specification.

XX Sequence 409 AA;

Query Match 2.9%; Score 11; DB 7; Length 409;

Best Local Similarity 100.0%; Pred. No. 0.11;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 341 ELPFVLMHPKP 351

Db 339 ELPFVLMHPKP 349

RESULT 13

ABG69496

ID ABG69496 standard; protein; 410 AA.

XX AC ABG69496;

XX DT 21-OCT-2002 (first entry)

XX DE Rat bait protein beta arrestin 2.

XX Rat; yeast two-hybrid assay; adipocyte; bait protein; NIDDM;
KW non-insulin diabetes mellitus; obesity; selected interacting domain; SID;
KW protein-protein interaction map; PIM; anorectic; metabolic disorder.

XX Rattus sp.
XX WO200253726-A2.
XX PN 11-JUL-2002.
XX PD 28-DEC-2001; 2001WO-EP015423.
XX PF 02-JAN-2001; 2001US-0259377P.
XX PR (HYBR-) HYBRIGENICS.
XX PA (CNRS) CENT NAT RECH SCI.
XX PI Legrain P, Marullo S, Jockers R;
XX PI WPI; 2002-583612/62.
XX DR N-PSDB; ABS51032.

XX PT Novel complex of protein-protein interactions in adipocyte cells for
PT identifying compounds that modulate the protein-protein interactions and
PT useful for treating obesity and metabolic disorders.
XX PS Claim 1; Page 53; 125pp; English.
XX The invention relates to a complex of protein-protein interactions
CC (forming a protein-protein interaction map, PIM) in adipocyte cells as
CC defined in the specification, or polynucleotides in adipocytes encoding
CC for the polypeptides. Also included are a recombinant cell expressing the
CC interacting polypeptides and a method of selecting a modulating compound
CC in adipocyte cells, by cultivating a recombinant host cell on a selective
CC medium containing a modulating compound and a reporter gene the
CC expression of which is toxic for the recombinant host cell which is
CC transformed with two vectors, where the first vector comprises a
CC polynucleotide encoding a first hybrid polypeptide and DNA binding domain
CC and the second vector comprising a polynucleotide encoding a second
CC hybrid polypeptide and an activating domain that activates the toxic
CC reporter gene, when the first and second hybrid polypeptides interact and
CC selecting the modulating compound which inhibits the growth of the

...LMLHPKP 350

2003 (first entry)
Rat Protein P29067, SEQ ID NO 4048

04003016475-A2.

14-AUG-2002; 2002WO-US025765.

01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.

(FARB) BAYER AG.

WPI; 2003-268312/26.
GENBANK; P29067.

New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
Claim 1; Page, 1017pp; English.

the invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment derivative or allelic variation of the nucleic acid sequence. Also, CC claimed are a vector comprising the novel polynucleotide, a host cell CC comprising the vector, a method for identifying a nucleotide sequence CC which is differentially regulated in an animal subjected to pain and a CC kit to perform the method, an array, a method for identifying an agent CC that increases or decreases the expression of the polynucleotide sequence CC that is differentially expressed in neuronal tissue of a first animal CC subjected to pain, a method for identifying a compound which regulates CC the expression of a polynucleotide sequence which is differentially CC expressed in an animal subjected to pain, a method for identifying a CC compound that regulates the activity of one or more of the CC polynucleotides, a method for producing a pharmaceutical composition, a

1940

```
Query Match      2.9%
Best Local Similarity 100.0%
Matches 11; Conservative 0; Mismatch 0; DB 7; Length 410;
```

QY	341	ELPFVLMHKKP	351	mismatches	0;	Indels	0;	Gaps	0;
	340	ELPFVLMHKKP	350						
Db									

RESULT 15	
ADE58181	
ID	
XX	standard, protein; 410 AA
AC	
AD	
AE	
AF	
AG	
AH	
AI	
AJ	
AK	
AL	
AM	
AN	
AO	
AP	
AQ	
AR	
AS	
AT	
AV	
AW	
AX	
AY	
AZ	
BA	
BB	
BC	
BD	
BE	
BF	
BG	
BH	
BI	
BJ	
BK	
BL	
BM	
BN	
BO	
BP	
BQ	
BR	
BS	
BT	
BV	
BW	
BX	
BY	
BZ	
CA	
CB	
CC	
CD	
CE	
CF	
CG	
CH	
CI	
CJ	
CK	
CL	
CM	
CN	
CO	
CP	
CQ	
CR	
CS	
CT	
CV	
CW	
CX	
CY	
CZ	
DA	
DB	
DC	
DD	
DE	
DF	
DG	
DH	
DI	
DJ	
DK	
DL	
DM	
DN	
DO	
DP	
DQ	
DR	
DS	
DT	
DV	
DW	
DX	
DY	
DZ	
EA	
EB	
EC	
ED	
EE	
EF	
EG	
EH	
EI	
EJ	
EK	
EL	
EM	
EN	
EO	
EP	
EQ	
ER	
ES	
ET	
EV	
EW	
EX	
EY	
EZ	
FA	
FB	
FC	
FD	
FE	
FF	
FG	
FH	
FI	
FJ	
FK	
FL	
FM	
FN	
FO	
FP	
FQ	
FR	
FS	
FT	
FV	
FW	
FX	
FY	
FZ	
GA	
GB	
GC	
GD	
GE	
GF	
GG	
GH	
GI	
GJ	
GK	
GL	
GM	
GN	
GO	
GP	
GQ	
GR	
GS	
GT	
GV	
GW	
GX	
GY	
GZ	
HA	
HB	
HC	
HD	
HE	
HF	
HG	
HH	
HI	
HJ	
HK	
HL	
HM	
HN	
HO	
HP	
HQ	
HR	
HS	
HT	
HV	
HW	
HX	
HY	
HZ	
IA	
IB	
IC	
ID	
IE	
IF	
IG	
IH	
II	
IJ	
IK	
IL	
IM	
IN	
IO	
IP	
IQ	
IR	
IS	
IT	
IV	
IW	
IX	
IY	
IZ	
JA	
JB	
JC	
JD	
JE	
JF	
JG	
JH	
JI	
JJ	
JK	
JL	
JM	
JN	
JO	
JP	
JQ	
JR	
JS	
JT	
JV	
JW	
JX	
JY	
JZ	
KA	
KB	
KC	
KD	
KE	
KF	
KG	
KH	
KI	
KJ	
KK	
KL	
KM	
KN	
KO	
KP	
KQ	
KR	
KS	
KT	
KV	
KW	
KX	
KY	
KZ	
LA	
LB	
LC	
LD	
LE	
LF	
LG	
LH	
LI	
LJ	
LK	
LL	
LM	
LN	

	XX	XX	DE
	2007	(First entry)	

Pat: no: 29067, SEQ ID NO 4052.

Rattus norvegicus. sciatic nerve laceration; sciatic nerve transection; sciatic nerve crush; sciatic nerve constriction injury; CCI; spared nerve injury; SNI; Chung.

MO2003016475-A2.

27-FEB-2003.

2002WO-US025765

01-NOV-2001; 2001US-0312147P
26-NOV-2001; 2001US-0346382P
2001US-0333347P.

(FARB) BAYER AG.

WPI; 2003-268312/26.
GENBANK; F29067.

New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.

CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates

CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (SNr)) in an animal (e.g. gene
CC injury (CCI) and spared nerve injury (SNr)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX

XX
SQ Sequence 410 AA;

Query Match 2.9%; Score 11; DB 7; Length 410;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 341 ELPFVLMHPKP 351
|||
Db 340 ELPFVLMHPKP 350

Search completed: February 9, 2005, 23:58:30
Job time : 166 secs

This Page Blank (uspto)

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 9, 2005, 23:55:44 ; Search time 43 Seconds
(without alignments)
664.897 Million cell updates/sec

Title: US-10-056-405-2
Perfect score: 383
Sequence: 1 MVYNFKVFKKCAPNGKVTLY.....ADVETPRQDTIDQASVDFE 383

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	2.9	382	4 US-09-880-137-8	Sequence 8, Appli
2	11	2.9	409	4 US-09-880-137-4	Sequence 4, Appli
3	11	2.9	409	4 US-09-880-137-7	Sequence 7, Appli
4	9	2.3	388	4 US-09-880-137-5	Sequence 5, Appli
5	9	2.3	388	4 US-09-880-137-6	Sequence 6, Appli
6	8	2.1	279	4 US-09-252-991A-27414	Sequence 27414, A
7	8	2.1	315	4 US-09-949-016-9940	Sequence 9940, Ap
8	8	2.1	401	4 US-09-949-016-8383	Sequence 8383, Ap
9	8	2.1	401	4 US-09-949-016-8384	Sequence 8384, Ap
10	8	2.1	410	4 US-09-880-137-3	Sequence 3, Appli
11	8	2.1	418	4 US-09-880-137-1	Sequence 1, Appli
12	8	2.1	418	4 US-09-880-137-2	Sequence 2, Appli
13	8	2.1	418	4 US-09-880-137-2	Sequence 2, Appli
14	7	1.8	15	2 US-08-484-905-28	Sequence 28, Appl
15	7	1.8	15	3 US-08-481-985B-28	Sequence 28, Appl
16	7	1.8	15	3 US-08-370-476-28	Sequence 28, Appl
17	7	1.8	15	3 US-08-992-877-8	Sequence 8, Appli
18	7	1.8	16	2 US-08-480-190-54	Sequence 54, Appl
19	7	1.8	16	2 US-08-488-379-54	Sequence 54, Appl
20	7	1.8	16	4 US-08-475-399A-54	Sequence 54, Appl
21	7	1.8	16	4 US-08-077-255A-54	Sequence 54, Appl
22	7	1.8	16	5 PCT-US93-07545-54	Sequence 54, Appl
23	7	1.8	19	4 US-09-423-097-4	Sequence 4, Appli
24	7	1.8	20	2 US-08-934-915-43	Sequence 43, Appl
25	7	1.8	20	2 US-08-934-915-81	Sequence 81, Appl
26	7	1.8	70	3 US-09-367-953B-28	Sequence 28, Appl
27	7	1.8	70	3 US-09-367-953B-29	Sequence 29, Appl
			7	3 US-09-367-953B-30	Sequence 30, Appl

28	7	1.8	70	3 US-09-367-953B-31	Sequence 31, Appl
29	7	1.8	70	3 US-09-367-953B-52	Sequence 52, Appl
30	7	1.8	70	3 US-09-367-953B-55	Sequence 55, Appl
31	7	1.8	70	3 US-09-367-953B-65	Sequence 65, Appl
32	7	1.8	70	3 US-09-367-953B-68	Sequence 68, Appl
33	7	1.8	70	3 US-09-367-953B-70	Sequence 70, Appl
34	7	1.8	70	3 US-09-367-953B-71	Sequence 71, Appl
35	7	1.8	70	3 US-09-367-953B-72	Sequence 72, Appl
36	7	1.8	70	3 US-09-367-953B-74	Sequence 74, Appl
37	7	1.8	70	3 US-09-367-953B-75	Sequence 75, Appl
38	7	1.8	70	3 US-09-367-953B-76	Sequence 76, Appl
39	7	1.8	70	3 US-09-367-953B-78	Sequence 78, Appl
40	7	1.8	70	3 US-09-367-953B-80	Sequence 80, Appl
41	7	1.8	70	3 US-09-367-953B-82	Sequence 82, Appl
42	7	1.8	70	3 US-09-367-953B-83	Sequence 83, Appl
43	7	1.8	70	3 US-09-367-953B-84	Sequence 84, Appl
44	7	1.8	70	3 US-09-367-953B-85	Sequence 85, Appl
45	7	1.8	70	3 US-09-367-953B-86	Sequence 86, Appl

ALIGNMENTS

RESULT 1
US-09-880-137-8
; Sequence 8, Application US/09880137
; Patent No. 6640025
; GENERAL INFORMATION:
; APPLICANT: Berstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; FILE REFERENCE: NMT-131
; CURRENT APPLICATION NUMBER: US/09/880,137
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186,706
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Homo sapiens mutation
US-09-880-137-8

Query Match 2.9%; Score 11; DB 4; Length 382;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 341 ELPFVLMHPKP 351
Db 339 ELPFVLMHPKP 349

RESULT 2
US-09-880-137-4
; Sequence 4, Application US/09880137
; Patent No. 6640025
; GENERAL INFORMATION:
; APPLICANT: Berstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; FILE REFERENCE: NMT-131
; CURRENT APPLICATION NUMBER: US/09/880,137
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186,706
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 409
; TYPE: PRT

ORGANISM: Homo sapiens
US-09-880-137-4

Query Match

Best Local Similarity 2.9%; Score 11; DB 4; Length 409;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 341 ELPFVLMHPKP 351
Db 339 ELPFVLMHPKP 349

RESULT 3

US-09-880-137-7
Sequence 7, Application US/09880137
Patent No. 6640025
GENERAL INFORMATION:
APPLICANT: Berstein, Gabriel
TITLE OF INVENTION: METHODS OF ASSAYING FOR G
FILE REFERENCE: MNI-131
CURRENT APPLICATION NUMBER: US/09/880,137
PRIOR FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: US 60/186,706
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 409
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Homo sapiens mutation
US-09-880-137-7

Query Match

Best Local Similarity 2.9%; Score 11; DB 4; Length 409;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 341 ELPFVLMHPKP 351
Db 339 ELPFVLMHPKP 349

RESULT 4

US-09-880-137-5
Sequence 5, Application US/09880137
Patent No. 6640025
GENERAL INFORMATION:
APPLICANT: Berstein, Gabriel
TITLE OF INVENTION: METHODS OF ASSAYING FOR G
FILE REFERENCE: MNI-131
CURRENT APPLICATION NUMBER: US/09/880,137
PRIOR FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: US 60/186,706
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 388
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-137-5

Query Match

Best Local Similarity 2.3%; Score 9; DB 4; Length 388;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 GKRDVVDHV 30
Db 19 GKRDVVDHV 27

RESULT 5

US-09-880-137-6
Sequence 6, Application US/09880137
Patent No. 6640025
GENERAL INFORMATION:
APPLICANT: Berstein, Gabriel
TITLE OF INVENTION: METHODS OF ASSAYING FOR G
FILE REFERENCE: MNI-131
CURRENT APPLICATION NUMBER: US/09/880,137
PRIOR FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: US 60/186,706
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 388
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-137-6

Query Match

Best Local Similarity 2.3%; Score 9; DB 4; Length 388;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 GKRDVVDHV 30
Db 19 GKRDVVDHV 27

RESULT 6

US-09-252-991A-27414
Sequence 27414, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 27414
LENGTH: 279
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27414

Query Match

Best Local Similarity 2.1%; Score 8; DB 4; Length 279;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 336 GELSAELP 343
Db 30 GELSAELP 37

RESULT 7

US-09-949-016-9940
Sequence 9940, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14

```
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9940
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9940
```

```
Query Match      2.1%; Score 8; DB 4; Length 315;
Best Local Similarity 100.0%; Pred. No. 20;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      22 GKRDFVDH 29
      |||||
Db      24 GKRDFVDH 31
```

RESULT 8

```
US-09-949-016-8383
; Sequence 8383, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8383
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8383
```

```
Query Match      2.1%; Score 8; DB 4; Length 401;
Best Local Similarity 100.0%; Pred. No. 24;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      22 GKRDFVDH 29
      |||||
Db      6 GKRDFVDH 13
```

RESULT 9

```
US-09-949-016-8384
; Sequence 8384, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
```

```
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8384
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8384
```

```
Query Match      2.1%; Score 8; DB 4; Length 401;
Best Local Similarity 100.0%; Pred. No. 24;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      22 GKRDFVDH 29
      |||||
Db      6 GKRDFVDH 13
```

RESULT 10

```
US-09-880-137-3
; Sequence 3, Application US/09880137
; Patent No. 6640025
; GENERAL INFORMATION:
; APPLICANT: Berstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; FILE REFERENCE: MNI-131
; CURRENT APPLICATION NUMBER: US/09/880,137
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186,706
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-137-3
```

```
Query Match      2.1%; Score 8; DB 4; Length 410;
Best Local Similarity 100.0%; Pred. No. 25;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      22 GKRDFVDH 29
      |||||
Db      23 GKRDFVDH 30
```

RESULT 11

```
US-09-880-137-1
; Sequence 1, Application US/09880137
; Patent No. 6640025
; GENERAL INFORMATION:
; APPLICANT: Berstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; FILE REFERENCE: MNI-131
; CURRENT APPLICATION NUMBER: US/09/880,137
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186,706
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-880-137-1
```

```
Query Match      2.1%; Score 8; DB 4; Length 418;
Best Local Similarity 100.0%; Pred. No. 25;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 22 GKRDVVDH 29
Db 23 GKRDVVDH 30

RESULT 12
US-09-880-137-2
; Sequence 2, Application US/09880137
; Patent No. 6640025
; GENERAL INFORMATION:
; APPLICANT: Berstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; FILE REFERENCE: NMI-131
; CURRENT APPLICATION NUMBER: US/09/880,137
; PRIOR APPLICATION NUMBER: 2001-03-05
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-137-2

Query Match
Best Local Similarity 2.1%; Score 8; DB 4; Length 418;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 22 GKRDVVDH 29
Db 23 GKRDVVDH 30

RESULT 13
US-08-484-905-28
; Sequence 28, Application US/08484905
; Patent No. 5976551
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; TITLE OF INVENTION: Kourilsky, Philippe
; TITLE OF INVENTION: An Altered Major Histocompatibility
; NUMBER OF INVENTION: Complex(MHC) Determinant and Methods for Using the
; NUMBER OF SEQUENCES: 127
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,905
; FILING DATE: 07-JUNE-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473
; FILING DATE: 15-NOV-1991
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E. R.

; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 03495.0106-03000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-905-28

Query Match
Best Local Similarity 1.8%; Score 7; DB 2; Length 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 256 LETSEGC 262
Db 1 LETSEGC 7

RESULT 14
US-08-481-985B-28
; Sequence 28, Application US/08481985B
; Patent No. 6011146
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; TITLE OF INVENTION: Altered Major Histocompatibility Complex
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,985B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473
; FILING DATE: 15-NOV-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03495.0106-04000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-481-985B-28

Query Match
1.8%; Score 7; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: February 10, 2005, 00:11:11
Job time : 44 secs

OY 256 LETSEGC 262
Db 1 LETSEGC 7

RESULT 15

US-08-370-476-28
; Sequence 28, Application US/08370476
; Patent No. 6153408
; GENERAL INFORMATION:
; APPLICANT: Motez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; APPLICANT: Lone, Yu-Chun
; APPLICANT: Ojcius, David
; APPLICANT: Cabrouge, Armada
; TITLE OF INVENTION: Altered Major Histocompatibility Complex
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 127
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flanagan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/370,476
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117,575
; FILING DATE: 07-SEP-1993
; APPLICATION NUMBER: US 08/072,787
; FILING DATE: 06-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473
; FILING DATE: 15-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 05243.0001-01000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-370-476-28

Query Match 1.8%; Score 7; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 256 LETSEGC 262
Db 1 LETSEGC 7

This Page Blank (uspto)

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 9, 2005, 23:58:40 ; Search time 131 Seconds
(without alignments)
952.245 Million cell updates/sec

Title: US-10-056-405-2
Perfect score: 383
Sequence: 1 MVYNFKVFKKCAPNGKVTLY.....ADVETFRQDTIDQASVDFE 383

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1373511 seqs, 325702437 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1373511

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	383	100.0	383 14	US-10-094-240-2	Sequence 2, Appli
2	383	100.0	383 14	US-10-056-405-2	Sequence 2, Appli
3	11	2.9	382 9	US-09-880-137-8	Sequence 8, Appli
4	11	2.9	382 10	US-09-800-137A-8	Sequence 8, Appli
5	11	2.9	398 14	US-10-094-240-25	Sequence 25, Appli
6	11	2.9	401 14	US-10-094-240-27	Sequence 27, Appli
7	11	2.9	409 9	US-09-880-137-4	Sequence 4, Appli
8	11	2.9	409 9	US-09-880-137-4	Sequence 7, Appli
9	11	2.9	409 10	US-09-800-137A-4	Sequence 4, Appli
10	11	2.9	409 10	US-09-800-137A-7	Sequence 7, Appli
11	11	2.9	410 14	US-10-038-010-54	Sequence 54, Appli
12	11	2.9	466 16	US-10-722-357-31	Sequence 31, Appli
13	9	2.3	388 9	US-09-880-137-5	Sequence 5, Appli

14	9	2.3	388 9	US-09-880-137-6	Sequence 6, Appli
15	9	2.3	388 10	US-09-800-137A-5	Sequence 5, Appli
16	9	2.3	388 10	US-09-800-137A-6	Sequence 6, Appli
17	8	2.1	38 9	US-09-864-761-40768	Sequence 40768, A
18	8	2.1	48 15	US-10-424-599-154582	Sequence 154582,
19	8	2.1	153 15	US-10-424-599-148204	Sequence 148204,
20	8	2.1	204 15	US-10-335-977-7580	Sequence 7580, Ap
21	8	2.1	208 16	US-10-767-701-41403	Sequence 41403, A
22	8	2.1	212 14	US-10-106-698-4673	Sequence 4673, Ap
23	8	2.1	235 15	US-10-424-599-224408	Sequence 224408,
24	8	2.1	270 16	US-10-767-701-38282	Sequence 38282, A
25	8	2.1	366 15	US-10-335-977-7581	Sequence 7581, Ap
26	8	2.1	410 9	US-09-880-137-3	Sequence 3, Appli
27	8	2.1	410 10	US-09-800-137A-3	Sequence 3, Appli
28	8	2.1	418 9	US-09-880-137-2	Sequence 1, Appli
29	8	2.1	418 9	US-09-880-137-2	Sequence 2, Appli
30	8	2.1	418 10	US-09-800-137A-1	Sequence 1, Appli
31	8	2.1	418 10	US-09-800-137A-2	Sequence 2, Appli
32	8	2.1	418 14	US-10-043-487-348	Sequence 348, App
33	8	2.1	448 9	US-09-815-242-11562	Sequence 11562, A
34	8	2.1	448 15	US-10-282-122A-58890	Sequence 58890, A
35	8	2.1	448 15	US-10-335-977-7582	Sequence 7582, Ap
36	8	2.1	452 14	US-10-038-010-52	Sequence 52, Appl
37	8	2.1	574 16	US-10-437-963-172259	Sequence 172259,
38	8	2.1	583 16	US-10-437-963-114326	Sequence 114326,
39	8	2.1	593 15	US-10-425-114-56486	Sequence 56486, A
40	8	2.1	662 15	US-10-282-122A-67739	Sequence 67739, A
41	7	1.8	16 14	US-10-062-710-116	Sequence 116, App
42	7	1.8	16 14	US-10-239-313A-196	Sequence 196, App
43	7	1.8	19 15	US-10-446-234-4	Sequence 4, Appli
44	7	1.8	57 15	US-10-424-599-200108	Sequence 200108,
45	7	1.8	59 15	US-10-424-599-267779	Sequence 267779,

ALIGNMENTS

RESULT 1
US-10-094-240-2
; Sequence 2, Application US/10094240
; Publication No. US20030082637A1
; GENERAL INFORMATION:
; APPLICANT: ZWIEBEL, LAURENCE J.
; TITLE OF INVENTION: ARRESTIN GENE, POLYPEPTIDE, AND METHODS OF USE THEREOF
; FILE REFERENCE: N8289
; CURRENT APPLICATION NUMBER: US/10/094,240
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 10/056,405
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/264,649
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Anopheles gambiae
US-10-094-240-2

Query Match	100.0%	Score 383;	DB 14;	Length 383;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 383;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MVYNFKVFKKCAPNGKVTLYMGKRDVDHVS	GVEPIDGIVLVLDDEYIRDNKRVFGQIVCS	60
DB	1	MVYNFKVFKKCAPNGKVTLYMGKRDVDHVS	GVEPIDGIVLVLDDEYIRDNKRVFGQIVCS	60
QY	61	FRYGRBEDEVMLNFQKELCLASEQIYRPEKS	DKQTKLQERLLKLGNSNAIPFTFNIS	120
DB	61	FRYGRBEDEVMLNFQKELCLASEQIYRPEKS	DKQTKLQERLLKLGNSNAIPFTFNIS	120
QY	121	PNAPSSVTLLQGEDDNGPCGVSYVKKFAGE	SETDRTHRRSTVTLGIRKIQAPTKQCG	180

```

Db      121 PNPSSVTLQGGEDDNGDPCGVSYVVKIPAGESETDRTHRSVTVLGIRKIQPAPTQCG 180
QY      181 OPCTLVKDFMLSGGELEVTLDKQLYLHGERIGVNICIRNNSNMKVKIKAMVQGGVD 240
Db      181 OPCTLVKDFMLSGGELEVTLDKQLYLHGERIGVNICIRNNSNMKVKIKAMVQGGVD 240
QY      241 VVLFQNGSYRNTVASLETSEGCPIQPGSSLOKVMYLTPLSSNKORRGIALDQIKRQDQ 300
Db      241 VVLFQNGSYRNTVASLETSEGCPIQPGSSLOKVMYLTPLSSNKORRGIALDQIKRQDQ 300
QY      301 CLASTTLLAQPDPDQDAFGVYISYAVKVKLFLGALGELSALPFLVLMHPKPGTKAKYIHA 360
Db      301 CLASTTLLAQPDPDQDAFGVYISYAVKVKLFLGALGELSALPFLVLMHPKPGTKAKYIHA 360
QY      361 DSQADVETFRQDTIIDQASVDPE 383
Db      361 DSQADVETFRQDTIIDQASVDPE 383

```

```

RESULT 2
US-10-056-405-2
; Sequence 2, Application US/10056405
; Publication No. US20030166013A1
; GENERAL INFORMATION:
; APPLICANT: ZWIEBEL, LAURENCE J.
; TITLE OF INVENTION: MOSQUITO OLFACATORY GENES, POLYPEPTIDES, AND METHODS OF
; FILE REFERENCE: N7841
; CURRENT APPLICATION NUMBER: US/10/056,405
; PRIOR FILING DATE: 2002-01-24
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Anopheles gambiae
US-10-056-405-2

```

```

Query Match
Best Local Similarity 100.0%; Score 383; DB 14; Length 383;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MVTNFKYFKKCAPNGKVTLYMGKRPVDVHSGVPEPIDGIVLDDDEYIRNRKVFQIVCS 60
Db      1 MVTNFKYFKKCAPNGKVTLYMGKRPVDVHSGVPEPIDGIVLDDDEYIRNRKVFQIVCS 60
QY      61 FRYGREDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLOERLKKLGSNAIPFTNIS 120
Db      61 FRYGREDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLOERLKKLGSNAIPFTNIS 120
QY      121 PNPSSVTLQGGEDDNGDPCGVSYVVKIPAGESETDRTHRSVTVLGIRKIQPAPTQCG 180
Db      121 PNPSSVTLQGGEDDNGDPCGVSYVVKIPAGESETDRTHRSVTVLGIRKIQPAPTQCG 180
QY      181 OPCTLVKDFMLSGGELEVTLDKQLYLHGERIGVNICIRNNSNMKVKIKAMVQGGVD 240
Db      181 OPCTLVKDFMLSGGELEVTLDKQLYLHGERIGVNICIRNNSNMKVKIKAMVQGGVD 240
QY      241 VVLFQNGSYRNTVASLETSEGCPIQPGSSLOKVMYLTPLSSNKORRGIALDQIKRQDQ 300
Db      241 VVLFQNGSYRNTVASLETSEGCPIQPGSSLOKVMYLTPLSSNKORRGIALDQIKRQDQ 300
QY      301 CLASTTLLAQPDPDQDAFGVYISYAVKVKLFLGALGELSALPFLVLMHPKPGTKAKYIHA 360
Db      301 CLASTTLLAQPDPDQDAFGVYISYAVKVKLFLGALGELSALPFLVLMHPKPGTKAKYIHA 360
QY      361 DSQADVETFRQDTIIDQASVDPE 383
Db      361 DSQADVETFRQDTIIDQASVDPE 383

```

```

RESULT 3
US-09-880-137-8
; Sequence 8, Application US/09880137
; Patent No. US20020031295A1
; GENERAL INFORMATION:
; APPLICANT: Berstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; FILE REFERENCE: MNI-131
; CURRENT APPLICATION NUMBER: US/09/880,137
; PRIOR FILING DATE: 2001-03-05
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Homo sapiens mutation
US-09-880-137-8

```

```

Query Match
Best Local Similarity 2.9%; Score 11; DB 9; Length 382;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      341 ELPEVLMHPKP 351
Db      339 ELPEVLMHPKP 349

```

```

RESULT 4
US-09-800-137A-8
; Sequence 8, Application US/09800137A
; Publication No. US20030157553A1
; GENERAL INFORMATION:
; APPLICANT: Berstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; FILE REFERENCE: MNI-131
; CURRENT APPLICATION NUMBER: US/09/800,137A
; PRIOR FILING DATE: 2001-03-05
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Homo sapiens mutation
US-09-800-137A-8

```

```

Query Match
Best Local Similarity 2.9%; Score 11; DB 10; Length 382;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      341 ELPEVLMHPKP 351
Db      339 ELPEVLMHPKP 349

```

```

RESULT 5
US-10-094-240-25
; Sequence 25, Application US/10094240
; Publication No. US20030082637A1
; GENERAL INFORMATION:
; APPLICANT: ZWIEBEL, LAURENCE J.
; TITLE OF INVENTION: ARRESTIN GENE, POLYPEPTIDE, AND METHODS OF USE THEREOF
; FILE REFERENCE: N8289
; CURRENT APPLICATION NUMBER: US/10/094,240

```

```
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 10/056,405
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/264,649
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 25
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Anopheles gambiae
US-10-094-240-25
```

```
Query Match          2.9%; Score 11; DB 14; Length 398;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      62 RYGREDEVMG 72
        |||||||
Db      61 RYGREDEVMG 71
```

RESULT 6

```
US-10-094-240-27
; Sequence 27, Application US/10094240
; Publication No. US20030082637A1
; GENERAL INFORMATION:
; APPLICANT: ZWIEBEL, LAURENCE J.
; TITLE OF INVENTION: ARRESTIN GENE, POLYPEPTIDE, AND METHODS OF USE THEREOF
; FILE REFERENCE: N8289
; CURRENT APPLICATION NUMBER: US/10/094,240
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 10/056,405
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/264,649
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 27
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-094-240-27
```

```
Query Match          2.9%; Score 11; DB 14; Length 401;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      62 RYGREDEVMG 72
        |||||||
Db      61 RYGREDEVMG 71
```

RESULT 7

```
US-09-880-137-4
; Sequence 4, Application US/09880137
; Patent No. US20020031295A1
; GENERAL INFORMATION:
; APPLICANT: Berstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
; FILE REFERENCE: MNI-131
; CURRENT APPLICATION NUMBER: US/09/880,137
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186,706
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-137-4
```

```
Query Match          2.9%; Score 11; DB 9; Length 409;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      341 ELPFVLMHPKP 351
        |||||||
Db      339 ELPFVLMHPKP 349
```

RESULT 8

```
US-09-880-137-7
; Sequence 7, Application US/09880137
; Patent No. US20020031295A1
; GENERAL INFORMATION:
; APPLICANT: Berstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
; FILE REFERENCE: MNI-131
; CURRENT APPLICATION NUMBER: US/09/880,137
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186,706
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Homo sapiens mutation
US-09-880-137-7
```

```
Query Match          2.9%; Score 11; DB 9; Length 409;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      341 ELPFVLMHPKP 351
        |||||||
Db      339 ELPFVLMHPKP 349
```

RESULT 9

```
US-09-800-137A-4
; Sequence 4, Application US/09800137A
; Publication No. US20030157553A1
; GENERAL INFORMATION:
; APPLICANT: Berstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
; FILE REFERENCE: MNI-131
; CURRENT APPLICATION NUMBER: US/09/800,137A
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186,706
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-800-137A-4
```

```
Query Match          2.9%; Score 11; DB 10; Length 409;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      341 ELPFVLMHPKP 351
        |||||||
Db      339 ELPFVLMHPKP 349
```

RESULT 10

US-09-800-137A-7
; Sequence 7, Application US/09800137A
; Publication No. US20030157553A1
; GENERAL INFORMATION:
; APPLICANT: Berstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; FILE REFERENCE: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
; CURRENT APPLICATION NUMBER: MNI-131
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186,706
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Homo sapiens mutation
US-09-800-137A-7

Query Match
Best Local Similarity 2.9%; Score 11; DB 10; Length 409;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 341 ELPFVLMHPKP 351
Db 339 ELPFVLMHPKP 349

RESULT 11
US-10-038-010-54
; Sequence 54, Application US/10038010
; Publication No. US20030040089A1
; GENERAL INFORMATION:
; APPLICANT: HYBRIGENICS
; APPLICANT: Pierre, Legrain
; TITLE OF INVENTION: Protein-protein interactions in adipocyte cells
; FILE REFERENCE: B4767A
; CURRENT APPLICATION NUMBER: US/10/038,010
; PRIOR FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 60/259,377
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: beta Arrestin2
; LOCATION: (1)..(410)
; OTHER INFORMATION:
US-10-038-010-54

Query Match
Best Local Similarity 2.9%; Score 11; DB 14; Length 410;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 341 ELPFVLMHPKP 351
Db 340 ELPFVLMHPKP 350

RESULT 12
US-10-722-357-31
; Sequence 31, Application US/10722357
; Publication No. US20040191803A1
; GENERAL INFORMATION:
; APPLICANT: GALLAGHER, MICHELA
; APPLICANT: LUND, PAULINE KAY
; APPLICANT: ROTHSTEIN, JEFFREY

; TITLE OF INVENTION: TARGET FOR THERAPY OF COGNITIVE IMPAIRMENT
; FILE REFERENCE: JHV-028.01
; CURRENT APPLICATION NUMBER: US/10/722,357
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: 60/413,152
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 31
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-722-357-31

Query Match
Best Local Similarity 2.9%; Score 11; DB 16; Length 466;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 341 ELPFVLMHPKP 351
Db 396 ELPFVLMHPKP 406

RESULT 13
US-09-880-137-5
; Sequence 5, Application US/09880137
; Patent No. US20020031295A1
; GENERAL INFORMATION:
; APPLICANT: Berstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; FILE REFERENCE: MNI-131
; CURRENT APPLICATION NUMBER: US/09/880,137
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186,706
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-137-5

Query Match
Best Local Similarity 2.3%; Score 9; DB 9; Length 388;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 GKRDFVDHV 30
Db 19 GKRDFVDHV 27

RESULT 14
US-09-880-137-6
; Sequence 6, Application US/09880137
; Patent No. US20020031295A1
; GENERAL INFORMATION:
; APPLICANT: Berstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; FILE REFERENCE: MNI-131
; CURRENT APPLICATION NUMBER: US/09/880,137
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186,706
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-137-6

Query Match 2.3%; Score 9; DB 9; Length 388;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 GKRDFFVDHV 30
Db 19 GKRDFFVDHV 27

RESULT 15

US-09-800-137A-5
; Sequence 5, Application US/09800137A
; Publication No. US20030157553A1
; GENERAL INFORMATION:
; APPLICANT: Berstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
; FILE REFERENCE: NMI-131
; CURRENT APPLICATION NUMBER: US/09/800,137A
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186,706
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-800-137A-5

Query Match 2.3%; Score 9; DB 10; Length 388;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 GKRDFFVDHV 30
Db 19 GKRDFFVDHV 27

Search completed: February 10, 2005, 00:13:29
Job time : 132 secs

This Page Blank (uspto)

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 9, 2005, 23:46:08 ; Search time 176 Seconds
(without alignments)
1114.354 Million cell updates/sec

Title: US-10-056-405-2

Perfect score: 383
Sequence: 1 MVTNFKVFKKCAPNGKVTLY.....ADVTFRQDTIDQASVDPE 383

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : UnlProt_03:*
1: unlprot_sprot:*
2: unlprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	383	100.0	383	2	Q95NPF3	Q95nf3 anopheles g
2	383	100.0	417	2	Q7PMG5	Q7pmg5 anopheles g
3	245	64.0	245	2	Q6VPP0	Q6vpp0 anopheles g
4	25	6.5	381	2	Q9B1G9	Q9b1g9 ascalaphus
5	20	5.2	364	1	ARRA_DROME	P15372 drosophila
6	18	4.7	18	2	Q7YTV9	Q7ytv9 anopheles s
7	18	4.7	18	2	Q7YTW0	Q7ytw0 anopheles p
8	18	4.7	18	2	Q7YTW1	Q7ytw1 anopheles a
9	17	4.4	363	1	ARR1_CALVI	P51486 calliphora
10	16	4.2	381	1	ARRH_HELVI	P55274 heliothis v
11	14	3.7	52	2	Q6X126	Q6x126 drosophila
12	13	3.4	400	1	ARRH_LIMPO	P51484 limulus pol
13	12	3.1	407	1	ARRH_LOCMI	P32122 locusta mig
14	11	2.9	217	2	Q68DZ5	Q68dz5 homo sapien
15	11	2.9	398	2	Q66GU6	Q66gu6 anopheles g
16	11	2.9	400	1	ARRB_CALVI	P51487 calliphora
17	11	2.9	401	1	ARRB_DROME	P19107 drosophila
18	11	2.9	401	1	ARRB_DROMI	P19108 drosophila
19	11	2.9	401	2	Q7Q5Q8	Q7q5q8 anopheles g
20	11	2.9	405	1	ARR2_ONCMY	P51467 oncorhynchu
21	11	2.9	406	2	Q6PEK2	Q6pek2 brachydanio
22	11	2.9	407	1	ARR1_ONCMY	P51466 oncorhynchu
23	11	2.9	408	2	Q6DFC4	Q6dfc4 xenopus lae
24	11	2.9	408	2	Q6GPY2	Q6gpy2 xenopus lae
25	11	2.9	408	2	Q7T2D2	Q7t2d2 brachydanio
26	11	2.9	409	1	ARR2_HUMAN	P32121 homo sapien
27	11	2.9	409	2	Q6ICT3	Q6ict3 homo sapien
28	11	2.9	410	1	ARR2_MOUSE	Q91y14 mus musculu
29	11	2.9	410	1	ARR2_RAT	P29067 rattus norv
30	11	2.9	415	1	ARR3_ONCMY	P51468 oncorhynchu
31	11	2.9	420	1	ARR2_BOVIN	P32120 bos taurus

32	10	2.6	147	2	Q6WGR2	Q6wgr2 metapenaeus
33	9	2.3	359	2	Q96EN2	Q96en2 homo sapien
34	9	2.3	388	1	ARRC_HUMAN	P36575 homo sapien
35	9	2.3	392	2	Q9N0H5	Q9n0h5 bos taurus
36	9	2.3	392	2	Q6NUV2	Q6nuv2 brachydanio
37	9	2.3	392	2	Q9PTE7	Q9pte7 ambystoma t
38	9	2.3	394	2	Q7YS78	Q7ys78 sus scrofa
39	9	2.3	412	2	Q641D8	Q641d8 xenopus lae
40	9	2.3	470	2	Q9V393	Q9v393 drosophila
41	9	2.3	1773	2	Q82745	Q82745 arabidopsis
42	8	2.1	141	2	Q48240	Q48240 dennyus dis
43	8	2.1	142	2	Q48239	Q48239 dennyus dis
44	8	2.1	143	2	Q48243	Q48243 dennyus car
45	8	2.1	147	2	Q48246	Q48246 dennyus sin

ALIGNMENTS

RESULT 1						
ID	Q95NPF3	PRELIMINARY;	PRT;	383	AA.	
AC	Q95NPF3;					
DT	01-DEC-2001 (TREMBLrel. 19, Created)					
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)					
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)					
DE	Arrestin.					
GN	Name=Arr1;					
OS	Anopheles gambiae (African malaria mosquito).					
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;					
OC	Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.					
OX	NCBI_TaxID=7165;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	TISSUE=Antennae, and Head;					
RX	MEDLINE=21680430; PubMed=11822731;					
RA	Merrill C.E., Riesgo-Escovar J., Pites R.J., Kafatos F.C.,					
RA	Carlson J.R., Zweibel L.J.;					
RT	"Visual arresting in olfactory pathways of Drosophila and the malaria					
RT	vector mosquito Anopheles gambiae.";					
RL	Proc. Natl. Acad. Sci. U.S.A. 99:1633-1638 (2002).					
DR	EMBL; AJ304409; CAC39103.2; -.					
DR	EMBL; AY017417; AAG54081.1; -.					
DR	HSSP; P17870; 1G4M.					
DR	GO; GO:0007600; P:sensory perception; IEA.					
DR	GO; GO:0007165; P:signal transduction; IEA.					
DR	InterPro; IPR000698; Arrestin.					
DR	InterPro; IPR011022; Arrestin_C.					
DR	InterPro; IPR011021; Arrestin_N.					
DR	Pfam; PF02752; Arrestin_C; 1.					
DR	Pfam; PF00339; Arrestin_N; 1.					
DR	PRINTS; PR00309; ARRESTIN.					
DR	PROSITE; PS00295; ARRESTINS; 1.					
DR	SEQUENCE 383 AA; 42809 MW; FA946438592BB53E CRC64;					
Query Match						
Best Local Similarity 100.0%; Score 383; DB 2; Length 383;						
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
QY	1	MVTNFKVFKKCAPNGKVTLYMGKRDVVDVHVGVEPIDGIIVLDDERYIRDRKVFQGIYCS	60			
DB	1	MVTNFKVFKKCAPNGKVTLYMGKRDVVDVHVGVEPIDGIIVLDDERYIRDRKVFQGIYCS	60			
QY	61	FRYGREDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLLKKLGSNAIPFTFNIS	120			

```
Db 61 FRYGREDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLKLKLGSMALPFTENIS 120
QY 121 PNAPSSVTLLQGGEDDNGDPCGVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQG 180
Db 121 PNAPSSVTLLQGGEDDNGDPCGVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQG 180
QY 181 QPCTLVRKDFMLSPGELELEVTLDKQLYLHGERIGVNICIRNNSNMKVKKIKAMVQGV 240
Db 181 QPCTLVRKDFMLSPGELELEVTLDKQLYLHGERIGVNICIRNNSNMKVKKIKAMVQGV 240
QY 241 VVLFQNGSYRNTVASLETSEGCPIQPGSSLQKVMYLLTPLSSNKQRCIALDQIKRQDQ 300
Db 241 VVLFQNGSYRNTVASLETSEGCPIQPGSSLQKVMYLLTPLSSNKQRCIALDQIKRQDQ 300
QY 301 CLASTTLLAQPDQDAFGVYIISYAVKVKLFLGALGGEISAEPLFVLMHPKPGTKAKVIHA 360
Db 301 CLASTTLLAQPDQDAFGVYIISYAVKVKLFLGALGGEISAEPLFVLMHPKPGTKAKVIHA 360
QY 361 DSQADVETFRQDTIDQASVD FE 383
Db 361 DSQADVETFRQDTIDQASVD FE 383
```

RESULT 2

```
Q7PMG5 PRELIMINARY; PRT; 417 AA.
ID Q7PMG5
AC Q7PMG5;
DT 01-MAR-2004 (Tremblrel. 26, Created)
DT 01-MAR-2004 (Tremblrel. 26, Last sequence update)
DE ENSANGP0000012569 (Fragment).
GN Name=ENSANGG0000010080;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxId=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAAB01008980; EAA13874.2; -.
DR HSSP; P17870; 1G4M.
DR GO; GO:0007600; P:sensory perception; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000698; Arrestin.
DR InterPro; IPR011022; Arrestin_C.
DR InterPro; IPR011021; Arrestin_N.
DR Pfam; PF02752; Arrestin_C; 1.
DR Pfam; PF00339; Arrestin_N; 1.
DR PRINTS; PR00309; ARRESTIN.
DR ProDom; PD002099; ARRESTIN.
DR PROSITE; PS00295; ARRESTIN; 1.
FT NON_TER 1
SQ SEQUENCE 417 AA; 46591 MW; 4EE98A3C32257FC0 CRC64;
```

Query Match

Best Local Similarity 100.0%; Score 383; DB 2; Length 417;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MVYNFKVFKKCAPNGKVTLLYMKRDFVDHVGVEPIDIGIVLDDDEYIRDNKRVFGIVCS 60
Db 35 MVYNFKVFKKCAPNGKVTLLYMKRDFVDHVGVEPIDIGIVLDDDEYIRDNKRVFGIVCS 60
QY 61 FRYGREDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLKLKLGSMALPFTENIS 120
Db 95 FRYGREDEVMGLNFQKELCLASEQIYPRPEKSDKEQTKLQERLKLKLGSMALPFTENIS 120
QY 121 PNAPSSVTLLQGGEDDNGDPCGVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQG 180
```

```
Db 155 PNAPSSVTLLQGGEDDNGDPCGVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQG 214
QY 181 QPCTLVRKDFMLSPGELELEVTLDKQLYLHGERIGVNICIRNNSNMKVKKIKAMVQGV 240
Db 215 QPCTLVRKDFMLSPGELELEVTLDKQLYLHGERIGVNICIRNNSNMKVKKIKAMVQGV 240
QY 241 VVLFQNGSYRNTVASLETSEGCPIQPGSSLQKVMYLLTPLSSNKQRCIALDQIKRQDQ 300
Db 275 VVLFQNGSYRNTVASLETSEGCPIQPGSSLQKVMYLLTPLSSNKQRCIALDQIKRQDQ 300
QY 301 CLASTTLLAQPDQDAFGVYIISYAVKVKLFLGALGGEISAEPLFVLMHPKPGTKAKVIHA 360
Db 335 CLASTTLLAQPDQDAFGVYIISYAVKVKLFLGALGGEISAEPLFVLMHPKPGTKAKVIHA 360
QY 361 DSQADVETFRQDTIDQASVD FE 383
Db 395 DSQADVETFRQDTIDQASVD FE 417
```

RESULT 3

```
Q6VPP0 PRELIMINARY; PRT; 245 AA.
ID Q6VPP0
AC Q6VPP0;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DE Arrestin (Fragment).
OS Anopheles gambiae (African malaria mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxId=7165;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=4ARR, Yaounde, and L3-5;
RA Morlais I., Poncon N., Simard F., Cohuet A., Fontenille D.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY333991; AAR01116.1; -.
DR EMBL; AY333992; AAR01117.1; -.
DR EMBL; AY333993; AAR01118.1; -.
DR EMBL; AY333995; AAR01120.1; -.
DR EMBL; AY333996; AAR01115.1; -.
DR EMBL; AY333994; AAR01121.1; -.
DR HSSP; P08168; 1AYR.
DR GO; GO:0007600; P:sensory perception; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000698; Arrestin.
DR InterPro; IPR011022; Arrestin_C.
DR InterPro; IPR011021; Arrestin_N.
DR Pfam; PF02752; Arrestin_C; 1.
DR Pfam; PF00339; Arrestin_N; 1.
DR PRINTS; PR00309; ARRESTIN.
DR ProDom; PD002099; ARRESTIN; 2.
FT NON_TER 1
SQ SEQUENCE 245 AA; 27038 MW; 86D8F4520115DA5F CRC64;
```

Query Match

Best Local Similarity 64.0%; Score 245; DB 2; Length 245;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 129 LQGGEDDNGDPCGVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQPCCTLVK 188
Db 1 LQGGEDDNGDPCGVSYVVKIFAGESETDRTHRSTVTLGIRKIQFAPTKQGQPCCTLVK 188
QY 189 DFMLSPEGELELEVTLDKQLYLHGERIGVNICIRNNSNMKVKKIKAMVQGV 248
Db 61 DFMLSPEGELELEVTLDKQLYLHGERIGVNICIRNNSNMKVKKIKAMVQGV 248
QY 249 YRNTVASLETSEGCPIQPGSSLQKVMYLLTPLSSNKQRCIALDQIKRQDCLASTTLL 308
Db 121 YRNTVASLETSEGCPIQPGSSLQKVMYLLTPLSSNKQRCIALDQIKRQDCLASTTLL 180
```

```

Qy 309 AOPDQDAFGVITISYAVKVKLFGLGGLGELSABLPLVLMHPKGTAKAVIHADSQADVET 368
      |||||
Db 181 AOPDQDAFGVITISYAVKVKLFGLGGLGELSABLPLVLMHPKGTAKAVIHADSQADVET 240

Qy 369 PRODT 373
      |||||
Db 241 PRODT 245

RESULT 4
Q9BIG9 ID Q9BIG9 PRELIMINARY; PRT; 381 AA.
AC Q9BIG9;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Arrestin.
GN Name=arx1;
OS Ascalaphus macaronius.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Neuroptera; Ascalaphidae; Ascalaphus.
OX NCBI_TaxId=146496;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Head;
RX MEDLINE=21184354; PubMed=11287006; DOI=10.1016/S0014-5793(01)02287-6;
RA Bentrop J., Schillo M., Gordon G., Draslar G., Paulsen R.;
RT "UV-light-dependent binding of a visual arrestin 1 isoform to
RT photoreceptor membranes in a neuropteran (Ascalaphus) compound eye.";
RL PEBs Lett. 493:112-116(2001).
DR EMBL; AJ303080; CAC36938.1; -.
DR HSSP; P17870; 1G4M.
DR GO; GO:0007600; P:sensory perception; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000698; Arrestin.
DR InterPro; IPR011022; Arrestin_C.
DR InterPro; IPR011021; Arrestin_N.
DR Pfam; PF02752; Arrestin_C; 1.
DR Pfam; PF00339; Arrestin_N; 1.
DR PRINTS; PRO0309; ARRESTIN.
DR PROSITE; PS00295; ARRESTINS; 1.
SQ SEQUENCE 381 AA; 42789 MW; 451DEF465969857D CRC64;

Query Match 6.5%; Score 25; DB 2; Length 381;
Best Local Similarity 100.0%; Pred. No. 5.9e-16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 RKVFGQIVCSFRYGREDEVMGINF 75
      |||||
Db 52 RKVFGQIVCSFRYGREDEVMGINF 76

RESULT 5
ARRA_DROME ID ARRA_DROME STANDARD; PRT; 364 AA.
AC P15372; Q9VJA8;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Phostrestin II (Arrestin A) (Arrestin 1).
GN Name=Arr1; Synonyms=ArrA; ORFNames=CG5711;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
RN [1]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RX MEDLINE=90138925; PubMed=1689056;
RA Smith D.P., Sheih B.-H., Zuker C.S.;
RT "Isolation and structure of an arrestin gene from Drosophila.";
RT Proc. Natl. Acad. Sci. U.S.A. 87:1003-1007(1990).

```

RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RX MEDLINE=20138926; PubMed=2105491;
 RA Hyde D.R., Mecklenburg K.L., Pollock J.A., Vithelec T.S., Benzer S.;
 RT "Twenty Drosophila visual system cDNA clones: one is a homolog of
 RT human arrestin.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:1008-1012(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers J.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriere S., Fleischmann W.,
 RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jatala M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kamos I., Simpson S., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RN [4]
 RP GENOME REANNOTATION.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Betencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley; TISSUE=Head;
 RX MEDLINE=22426066; PubMed=12537569;
 RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
 RA George R.A., Guarini H., Krommiller B., Pacleb J.M., Park S., Wan K.H.,
 RA Rubin G.M., Celniker S.E.;
 RT "A Drosophila full-length cDNA resource.";
 RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
 RN [6]
 RP PHOSPHORYLATION.

RX MEDLINE=91282780; PubMed=1905538;
RA Matsumoto H., Yamada T.;
RT "Phosrestins I and II: arrestin homologs which undergo differential
RT light-induced phosphorylation in the Drosophila photoreceptor in
RT vivo.";
RL Biochem. Biophys. Res. Commun. 177:1306-1312(1991).
RN [7]
RP FUNCTION.
RX MEDLINE=93303590; PubMed=8316831;
RA Dolph P.J., Ranganathan R., Colley N.J., Hardy R.W., Socolich M.,
RA Zuker C.S.;
RT "Arrestin function in inactivation of G protein-coupled receptor
RT rhodopsin in vivo.";
RL Science 260:1910-1916(1993).
CC -1- FUNCTION: Regulates photoreceptor cell deactivation. Arr1 and Arr2
CC proteins are mediators of rhodopsin inactivation and are essential
CC for the termination of the phototransduction cascade.
CC -1- TISSUE SPECIFICITY: Expressed specifically and abundantly in the
CC photoreceptors. Inner and outer segments, and the inner plexiform
CC regions of the retina.
CC -1- PTM: Phosphorylated, but does not undergo light-induced
CC phosphorylation.
CC -1- SIMILARITY: Belongs to the arrestin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M30177; -; NOT ANNOTATED_CDS.
DR EMBL; M30140; AAA28380.1; -
DR EMBL; AE003657; AAF53644.1; -
DR EMBL; AY061824; AAL27635.1; -
DR PIR; A34867; A34867.
DR HSSP; P17870; 1G4M.
DR IntAct; P15372; -
DR FlyBase; FBgn0000120; Arr1.
DR GO; GO:0005624; C:membrane fraction; IDA.
DR GO; GO:0016028; C:rhododerm; IDA.
DR GO; GO:0016060; P:metarhodopsin inactivation; IGI.
DR InterPro; IPR000698; Arrestin.
DR InterPro; IPR011022; Arrestin_C.
DR InterPro; IPR011021; Arrestin_N.
DR Pfam; PF02752; Arrestin_C; 1.
DR Pfam; PF00339; Arrestin_N; 1.
DR PRINTS; PR00309; ARRESTIN.
DR PRODOM; PD002099; Arrestin; 2.
DR PROSITE; PS00295; ARRESTINS; 1.
KW Phosphorylation; Sensory transduction; Vision.
SQ SEQUENCE 364 AA; 40771 MW; 0DCC764C4F890FC2 CRC64;

Query Match
Best Local Similarity 5.2%; Score 20; DB 1; Length 364;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 VKKIKAMVQGVVLLFQNG 247
Db |||||
227 VKKIKAMVQGVVLLFQNG 246

RESULT 6
ID Q7YTV9 PRELIMINARY; PRT; 18 AA.
AC Q7YTV9;
DT 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DE Arrestin (Fragment).
GN Name=arr1;
OS Anopheles stephensi (Indo-Pakistan malaria mosquito).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=30069;
RN [1]
RP SEQUENCE FROM N.A.
RA Favia G., Ricci I., Casiraghi M., Esposito F.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ544225; CAD66651.1; -
FT NON TER 18
SQ SEQUENCE 18 AA; 2075 MW; A273A394A2A6EF66 CRC64;

Query Match
Best Local Similarity 4.7%; Score 18; DB 2; Length 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVYNFKVFKKCAPNGKVT 18
Db |||||
1 MVYNFKVFKKCAPNGKVT 18

RESULT 7
ID Q7YTWO PRELIMINARY; PRT; 18 AA.
AC Q7YTWO;
DT 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DE Arrestin (Fragment).
GN Name=arr1;
OS Anopheles pharoensis.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=221566;
RN [1]
RP SEQUENCE FROM N.A.
RA Favia G., Ricci I., Casiraghi M., Esposito F.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ544225; CAD66650.1; -
FT NON TER 18
SQ SEQUENCE 18 AA; 2075 MW; A273A394A2A6EF66 CRC64;

Query Match
Best Local Similarity 4.7%; Score 18; DB 2; Length 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVYNFKVFKKCAPNGKVT 18
Db |||||
1 MVYNFKVFKKCAPNGKVT 18

RESULT 8
ID Q7YTW1 PRELIMINARY; PRT; 18 AA.
AC Q7YTW1;
DT 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DE Arrestin (Fragment).
GN Name=arr1;
OS Anopheles arabiensis (Mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=7173;
RN [1]
RP SEQUENCE FROM N.A.
RA Favia G., Ricci I., Casiraghi M., Esposito F.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ544224; CAD66649.1; -
FT NON TER 18
SQ SEQUENCE 18 AA; 2075 MW; A273A394A2A6EF66 CRC64;

Query Match
Best Local Similarity 4.7%; Score 18; DB 2; Length 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVYNFKVFKKCAPNGKVT 18
Db |||||
1 MVYNFKVFKKCAPNGKVT 18

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MVYNFKVFKKCAPNGKVT 18
 DB 1 MVYNFKVFKKCAPNGKVT 18

RESULT 9

ARR1_CALVI STANDARD; PRT; 363 AA.
 AC P51486;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Phoreactin II (Arrestin A) (Arrestin 1).
 GN Name=ARR1;
 OS Calliphora vicina (Blue blowfly) (Calliphora erythrocephala).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Calliphoridae; Calliphora.
 OX NCBI_TaxID=7373;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Retina;
 RX MEDLINE=95014564; PubMed=7929436;
 RA Plangger A., Malicki D., Whitney M., Paulsen R.;
 RT "Mechanism of arrestin 2 function in rhabdomic photoreceptors."
 RL J. Biol. Chem. 269:26969-26975(1994).
 CC -1- SIMILARITY: Belongs to the arrestin family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X79072; CAA55672.1; -.
 DR PIR; A55081; A55081.
 DR HSSP; P17870; IG4M.
 DR InterPro; IPR000698; Arrestin.
 DR InterPro; IPR011022; Arrestin_C.
 DR InterPro; IPR011021; Arrestin_N.
 DR Pfam; PF02752; Arrestin_C; 1.
 DR Pfam; PF00339; Arrestin_N; 1.
 DR PRINTS; PR00309; ARRESTIN.
 DR PRODOM; PD002099; Arrestin; 2.
 DR PROSITE; PS00295; ARRESTINS; 1.
 KW Sensory transduction; Vision.
 SQ SEQUENCE 363 AA; 40680 MW; 7C345D818E46C23E CRC64;

Query Match 4.4%; Score 17; DB 1; Length 363;
 Best Local Similarity 100.0%; Pred. No. 5.9e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 322 SYAVKVKLFLGALGSEL 338
 DB 321 SYAVKVKLFLGALGSEL 337

RESULT 10

ARRH_HELVI STANDARD; PRT; 381 AA.
 AC P55274;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Arrestin homolog.
 OS Heliothis virescens (Noctuid moth) (Owlet moth).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
 OC Noctuidae; Heliothinae; Heliothis.

OX NCBI_TaxID=7102;

RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Antenna;
 RX MEDLINE=93199955; PubMed=8452755; DOI=10.1016/0898-6568(93)90009-B;
 RA Raming K., Freitag J., Krieger J., Breer H.;
 RT "Arrestin-subtypes in insect antennae."
 RL Cell. Signal. 5:69-80(1993).
 CC -1- SIMILARITY: Belongs to the arrestin family.
 CC PIR; B56607; B56607.
 DR HSSP; P17870; IG4M.
 DR InterPro; IPR000698; Arrestin.
 DR InterPro; IPR011022; Arrestin_C.
 DR InterPro; IPR011021; Arrestin_N.
 DR Pfam; PF02752; Arrestin_C; 1.
 DR Pfam; PF00339; Arrestin_N; 1.
 DR PRINTS; PR00309; ARRESTIN.
 DR PRODOM; PD002099; Arrestin; 2.
 DR PROSITE; PS00295; ARRESTINS; 1.
 KW Sensory transduction.
 SQ SEQUENCE 381 AA; 42747 MW; 84BB92B1BB3DA573 CRC64;

Query Match 4.2%; Score 16; DB 1; Length 381;
 Best Local Similarity 100.0%; Pred. No. 6.2e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MVYNFKVFKKCAPNGK 16
 DB 1 MVYNFKVFKKCAPNGK 16

RESULT 11

Q6X126 PRELIMINARY; PRT; 52 AA.
 ID Q6X126
 AC Q6X126;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Similar to Drosophila melanogaster CG5711 (Fragment).
 OS Drosophila yakuba (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7245;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22887302; PubMed=14525923; DOI=10.1101/gr.1311003;
 RA Domazet-Lošo T., Tautz D.;
 RT "An evolutionary analysis of orphan genes in Drosophila."
 RL Genome Res. 13:2213-2219(2003).
 DR EMBL; AY232006; AAR10029.1; -.
 DR HSSP; P08168; IAYR.
 DR GO; GO:0007600; P:sensory perception; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR000698; Arrestin.
 DR PRODOM; PD002099; Arrestin; 1.
 DR NON_TER 1
 FT NON_TER 1
 FT NON_TER 52
 SQ SEQUENCE 52 AA; 6166 MW; 081C148570B5EB6F CRC64;

Query Match 3.7%; Score 14; DB 2; Length 52;
 Best Local Similarity 100.0%; Pred. No. 1.2e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 33 VEPIDGIVLDDEY 46
 DB 33 VEPIDGIVLDDEY 46

RESULT 12

ARRH_LIMPO STANDARD; PRT; 400 AA.
 ID ARR1_LIMPO
 AC P51484;


```

DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Arrestin, lateral eye.
OS Limulus polyphemus (Atlantic horseshoe crab).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
OC Limulidae; Limulus.
OX NCBI_TaxId=6850;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=95096819; PubMed=7798902;
RA Smith W.C., Greenberg R.M., Calman B.G., Hendrix M.M., Hutchinson L.,
RA Donoso L.A., Batteille B.-A.;
RT "Isolation and expression of an arrestin cDNA from the horseshoe crab
RT lateral eye.";
RL J. Neurochem. 64:1-13(1995).
CC -1- FUNCTION: Plays an important role in the photoreceptor
CC transduction.
CC -1- PTM: Phosphorylated.
CC -1- SIMILARITY: Belongs to the arrestin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U08883; AAA82007.1; -
DR HSSP; P17870; 1G4M.
DR InterPro; IPR000698; Arrestin.
DR InterPro; IPR011022; Arrestin_C.
DR InterPro; IPR011021; Arrestin_N.
DR Pfam; PF02752; Arrestin_C; 1.
DR Pfam; PF00339; Arrestin_N; 1.
DR PRINTS; PR00309; ARRESTIN.
DR ProDom; PD002099; Arrestin; 2.
DR PROSITE; PS00295; ARRESTINS; 1.
DR Phosphorylation; Sensory transduction; Vision.
SQ SEQUENCE 400 AA; 44302 MW; F30D0D25BC2BEE33 CRC64;

Query Match
Best Local Similarity 3.4%; Score 13; DB 1; Length 400;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 FRYGREDEVWGL 73
Db 68 FRYGREDEVWGL 80

RESULT 13
ARRH LOCM1
ID ARRH LOCM1 STANDARD; PRT; 407 AA.
AC P32122;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Arrestin homolog.
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxId=7004;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Antenna;
RX MEDLINE=9319955; PubMed=8452755; DOI=10.1016/0898-6568(93)90009-B;
RA Raming K., Freitag J., Krieger J., Breer H.;
RT "Arrestin-subtypes in insect antennae.";
RL Cell. Signal. 5:69-80(1993).
CC -1- SIMILARITY: Belongs to the arrestin family.

```

```

CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; S57174; AAB25860.1; -
DR PIR; A56607; A56607.
DR HSSP; P17870; 1G4M.
DR InterPro; IPR000698; Arrestin.
DR InterPro; IPR011022; Arrestin_C.
DR InterPro; IPR011021; Arrestin_N.
DR Pfam; PF02752; Arrestin_C; 1.
DR Pfam; PF00339; Arrestin_N; 1.
DR PRINTS; PR00309; ARRESTIN.
DR ProDom; PD002099; Arrestin; 2.
DR PROSITE; PS00295; ARRESTINS; 1.
DR Sensory transduction.
SQ SEQUENCE 407 AA; 45543 MW; DEC28A3A534935BB CRC64;

Query Match
Best Local Similarity 3.1%; Score 12; DB 1; Length 407;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 RYGREDEVWGL 73
Db 69 RYGREDEVWGL 80

RESULT 14
ID Q68DZ5 PRELIMINARY; PRT; 217 AA.
AC Q68DZ5;
DT 25-OCT-2004 (TRENBLREL. 28, Created)
DT 25-OCT-2004 (TRENBLREL. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLREL. 28, Last annotation update)
DE Hypothetical protein DKFZp686L0365.
GN Name=DKFZp686L0365;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Endometrium;
RG The German cDNA Consortium;
RA Ottenwaelder B., Obermaier B., Deutschenbaur S., Schaipp A.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR749218; CAH18075.1; -
DR InterPro; IPR000698; Arrestin.
DR InterPro; IPR011022; Arrestin_C.
DR Pfam; PF02752; Arrestin_C; 1.
DR ProDom; PD002099; Arrestin; 1.
DR Hypothetical protein.
SQ SEQUENCE 217 AA; 24362 MW; 61653F5BACB80FD CRC64;

Query Match
Best Local Similarity 2.9%; Score 11; DB 2; Length 217;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 341 ELPFVLMHPKP 351
Db 147 ELPFVLMHPKP 157

RESULT 15
ID Q66GU6 PRELIMINARY; PRT; 398 AA.
AC Q66GU6;

```


DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Arrestin 2-like protein Arr2.
GN Name=ARR2;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RX MEDLINE=23159591; PubMed=14986925;
RA Merril C.E., Plets R.J., Zwiebel L.J.;
RT "Molecular characterization of arrestin family members in the malaria
vector mosquito, Anopheles gambiae.";
RL Insect Mol. Biol. 12:641-650(2003).
DR EMBL; BK000996; DAA00888.1; -.
DR InterPro; IPR006698; Arrestin.
DR InterPro; IPR011022; Arrestin_C.
DR InterPro; IPR011021; Arrestin_N.
DR Pfam; PF02752; Arrestin_C; 1.
DR Pfam; PF00339; Arrestin_N; 1.
DR PRINTS; PR00309; ARRESTIN.
DR ProDom; PD002099; Arrestin; 2.
DR PROSITE; PS00295; ARRESTINS; 1.
SQ SEQUENCE 398 AA; 44536 MW; 73DD73FB34F01418 CRC64;

Query Match 2.9%; Score 11; DB 2; Length 398;
Best Local Similarity 100.0%; Pred. No. 0.066;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 62 RYGREBDEVMG 72
|||
Db 61 RYGREBDEVMG 71

Search completed: February 10, 2005, 00:01:31
Job time : 177 secs

This page Blank (uspto)

This page Blank (uspto)